

## TITLE OF THE INVENTION

MU-CONOPEPTIDES

## CROSS-REFERENCE TO RELATED APPLICATIONS

5 [0001] The present application claims benefit under 35 USC §119(e) to U.S. provisional patent applications Serial No. 60/219,619 filed on 21 July 2000, Serial No. 60/245,157 filed on 3 November 2000, Serial No. 60/264,319 filed on 29 January 2001 and Serial No. 60/277,270 filed on 21 March 2001. Each of these applications is incorporated herein by reference.

10 [0002] This invention was made with Government support under Grant No. PO1 GM48677 awarded by the National Institute of General Medical Sciences, National Institutes of Health, Bethesda, Maryland. The United States Government has certain rights in the invention.

## BACKGROUND OF THE INVENTION

20 [0003] The present invention is to  $\mu$ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the  $\mu$ -conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The  $\mu$ -conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the  $\mu$ -conopeptides and encoding propeptides, as well as the propeptides.

25 [0004] The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are incorporated by reference, and for convenience are referenced in the following text by author and date and are listed alphabetically by author in the appended bibliography.

30 [0005] *Conus* is a genus of predatory marine gastropods (snails) which envenomate their prey. Venomous cone snails use a highly developed projectile apparatus to deliver their cocktail of toxic conotoxins into their prey. In fish-eating species such as *Conus magus* the cone detects the presence of the fish using chemosensors in its siphon and when close enough extends its proboscis and fires a hollow harpoon-like tooth containing venom into the fish. This immobilizes the fish and enables the cone snail to wind it into its mouth via an attached filament. For general information on *Conus* and their venom see the website address

<http://grimwade.biochem.unimelb.edu.au/cone/referenc.html>. Prey capture is accomplished through a sophisticated arsenal of peptides which target specific ion channel and receptor subtypes. Each *Conus* species venom appears to contain a unique set of 50-200 peptides. The composition of the venom differs greatly between species and between individual snails within each species, each optimally evolved to paralyse its prey. The active components of the venom are small peptide toxins, typically 10-40 amino acid residues in length and are typically highly constrained peptides due to their high density of disulphide bonds.

[0006] The venoms consist of a large number of different peptide components that when separated exhibit a range of biological activities: when injected into mice they elicit a range of physiological responses from shaking to depression. The paralytic components of the venom that have been the focus of recent investigation are the  $\alpha$ -,  $\omega$ - and  $\mu$ -conotoxins. All of these conotoxins act by preventing neuronal communication, but each targets a different aspect of the process to achieve this. The  $\alpha$ -conotoxins target nicotinic ligand gated channels, the  $\mu$ -conotoxins target the voltage-gated sodium channels and the  $\omega$ -conotoxins target the voltage-gated calcium channels (Olivera et al., 1985; Olivera et al., 1990). For example a linkage has been established between  $\alpha$ -,  $\alpha A$ - &  $\phi$ -conotoxins and the nicotinic ligand-gated ion channel;  $\omega$ -conotoxins and the voltage-gated calcium channel;  $\mu$ -conotoxins and the voltage-gated sodium channel;  $\delta$ -conotoxins and the voltage-gated sodium channel;  $\kappa$ -conotoxins and the voltage-gated potassium channel; conantokins and the ligand-gated glutamate (NMDA) channel.

[0007] However, the structure and function of only a small minority of these peptides have been determined to date. For peptides where function has been determined, three classes of targets have been elucidated: voltage-gated ion channels; ligand-gated ion channels, and G-protein-linked receptors.

[0008] *Conus* peptides which target voltage-gated ion channels include those that delay the inactivation of sodium channels, as well as blockers specific for sodium channels, calcium channels and potassium channels. Peptides that target ligand-gated ion channels include antagonists of NMDA and serotonin receptors, as well as competitive and noncompetitive nicotinic receptor antagonists. Peptides which act on G-protein receptors include neurotensin and vasopressin receptor agonists. The unprecedented pharmaceutical selectivity of conotoxins is at least in part defined by a specific disulfide bond frameworks combined with hypervariable amino acids within disulfide loops (for a review see McIntosh et al., 1998).

[0009] There are drugs used in the treatment of pain, which are known in the literature and to the skilled artisan. See, for example, Merck Manual, 16th Ed. (1992). However, there is a demand for more active analgesic agents with diminished side effects and toxicity and which are non-addictive. The ideal analgesic would reduce the awareness of pain, produce analgesia over a wide range of pain types, act satisfactorily whether given orally or parenterally, produce minimal or no side effects, be free from tendency to produce tolerance and drug dependence.

[0010] Due to the high potency and exquisite selectivity of the conopeptides, several are in various stages of clinical development for treatment of human disorders. For example, two *Conus* peptides are being developed for the treatment of pain. The most advanced is  $\omega$ -conotoxin MVIIA (ziconotide), an N-type calcium channel blocker (see Heading, C., 1999; U.S. Patent No. 5,859,186).  $\omega$ -Conotoxin MVIIA, isolated from *Conus magus*, is approximately 1000 times more potent than morphine, yet does not produce the tolerance or addictive properties of opiates.  $\omega$ -Conotoxin MVIIA has completed Phase III (final stages) of human clinical trials and has been approved as a therapeutic agent.  $\omega$ -Conotoxin MVIIA is introduced into human patients by means of an implantable, programmable pump with a catheter threaded into the intrathecal space. Preclinical testing for use in post-surgical pain is being carried out on another *Conus* peptide, contulakin-G, isolated from *Conus geographus* (Craig et al. 1999). Contulakin-G is a 16 amino acid O-linked glycopeptide whose C-terminus resembles neurotensin. It is an agonist of neurotensin receptors, but appears significantly more potent than neurotensin in inhibiting pain in *in vivo* assays.

[0011] In view of a large number of biologically active substances in *Conus* species it is desirable to further characterize them and to identify peptides capable of treating disorders involving voltage gated ion channels, such as stroke and pain. Surprisingly, and in accordance with this invention, Applicants have discovered novel conotoxins that can be useful for the treatment of disorders involving voltage gated ion channels and could address a long felt need for a safe and effective treatment.

#### SUMMARY OF THE INVENTION

[0012] The present invention is to  $\mu$ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the  $\mu$ -conopeptides or derivatives are

useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The  $\mu$ -conopeptides are also useful for treating neuromuscular disorders. The invention is further directed to nucleic acid sequences encoding the  $\mu$ -conopeptides and encoding propeptides, as well as the propeptides.

5 [0013] More specifically, the present invention is directed to  $\mu$ -conopeptides, having the amino acid sequences set forth in Tables 1 and 2 below.

[0014] The present invention is also directed to derivatives or pharmaceutically acceptable salts of the  $\mu$ -conopeptides or the derivatives. Examples of derivatives include peptides in which the Arg residues may be substituted by Lys, ornithine, homoargine, nor-Lys, 10 N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any synthetic basic amino acid; the Lys residues may be substituted by Arg, ornithine, homoargine, nor-Lys, or any synthetic basic amino acid; the Tyr residues may be substituted with meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any synthetic hydroxy containing amino acid; the Ser residues may be substituted with Thr or any synthetic hydroxylated amino acid; the Thr residues may be substituted with Ser or any synthetic hydroxylated amino acid; the Phe residues may be substituted with any synthetic aromatic amino acid; the Trp residues may be substituted with Trp (D), neo-Trp, halo-Trp (D or L) or any aromatic synthetic amino acid; and the Asn, Ser, Thr or Hyp residues may be glycosylated. The halogen may be iodo, chloro, 15 fluoro or bromo; preferably iodo for halogen substituted-Tyr and bromo for halogen-substituted Trp. The Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho- and O-phospho-derivatives. The acidic amino acid residues may be substituted with any synthetic acidic amino acid, e.g., tetrazolyl derivatives of Gly and Ala. The aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains  $C_nH_{2n+2}$  up to and 20 including  $n=8$ . The Met residues may be substituted by norleucine (Nle). The Cys residues may be in D or L configuration and may optionally be substituted with homocysteine (D or L).

[0015] Examples of synthetic aromatic amino acid include, but are not limited to, nitro-Phe, 4-substituted-Phe wherein the substituent is  $C_1$ - $C_3$  alkyl, carboxyl, hydroxymethyl, sulphomethyl, halo, phenyl, -CHO, -CN, -SO<sub>3</sub>H and -NHAc. Examples of synthetic hydroxy 30 containing amino acid, include, but are not limited to, such as 4-hydroxymethyl-Phe, 4-hydroxyphenyl-Gly, 2,6-dimethyl-Tyr and 5-amino-Tyr. Examples of synthetic basic amino acids include, but are not limited to, N-1-(2-pyrazoliny)-Arg, 2-(4-piperiny)-Gly, 2-(4-

piperinyl)-Ala, 2-[3-(2S)pyrrolinyl)-Gly and 2-[3-(2S)pyrrolinyl)-Ala. These and other synthetic basic amino acids, synthetic hydroxy containing amino acids or synthetic aromatic amino acids are described in Building Block Index, Version 3.0 (1999 Catalog, pages 4-47 for hydroxy containing amino acids and aromatic amino acids and pages 66-87 for basic amino acids; see also <http://www.amino-acids.com>), incorporated herein by reference, by and available from RSP Amino Acid Analogues, Inc., Worcester, MA. Examples of synthetic acid amino acids include those derivatives bearing acidic functionality, including carboxyl, phosphate, sulfonate and synthetic tetrazolyl derivatives such as described by Ornstein et al. (1993) and in U.S. Patent No. 5,331,001, each incorporated herein by reference.

[0016] Optionally, in the  $\mu$ -conopeptides of the present invention, the Asn residues may be modified to contain an N-glycan and the Ser, Thr and Hyp residues may be modified to contain an O-glycan (e.g., g-N, g-S, g-T and g-Hyp). In accordance with the present invention, a glycan shall mean any N-, S- or O-linked mono-, di-, tri-, poly- or oligosaccharide that can be attached to any hydroxy, amino or thiol group of natural or modified amino acids by synthetic or enzymatic methodologies known in the art. The monosaccharides making up the glycan can include D-allose, D-altrose, D-glucose, D-mannose, D-gulose, D-idose, D-galactose, D-talose, D-galactosamine, D-glucosamine, D-N-acetyl-glucosamine (GlcNAc), D-N-acetyl-galactosamine (GalNAc), D-fucose or D-arabinose. These saccharides may be structurally modified, e.g., with one or more O-sulfate, O-phosphate, O-acetyl or acidic groups, such as sialic acid, including combinations thereof. The glycan may also include similar polyhydroxy groups, such as D-penicillamine 2,5 and halogenated derivatives thereof or polypropylene glycol derivatives. The glycosidic linkage is beta and 1-4 or 1-3, preferably 1-3. The linkage between the glycan and the amino acid may be alpha or beta, preferably alpha and is 1-.

[0017] Core O-glycans have been described by Van de Steen et al. (1998), incorporated herein by reference. Mucin type O-linked oligosaccharides are attached to Ser or Thr (or other hydroxylated residues of the present peptides) by a GalNAc residue. The monosaccharide building blocks and the linkage attached to this first GalNAc residue define the "core glycans," of which eight have been identified. The type of glycosidic linkage (orientation and connectivities) are defined for each core glycan. Suitable glycans and glycan analogs are described further in U.S. Serial No. 09/420,797 filed 19 October 1999 and in PCT Application No. PCT/US99/24380 filed 19 October 1999 (PCT Published Application No. WO 00/23092), each incorporated herein by reference. A preferred glycan is Gal( $\beta$ 1 $\rightarrow$ 3)GalNAc( $\alpha$ 1 $\rightarrow$ ).

[0018] Optionally, in the  $\mu$ -conopeptides described above, pairs of Cys residues may be replaced pairwise with isoteric lactam or ester-thioether replacements, such as Ser/(Glu or Asp), Lys/(Glu or Asp), Cys/(Glu or Asp) or Cys/Ala combinations. Sequential coupling by known methods (Barnay et al., 2000; Hruby et al., 1994; Bitan et al., 1997) allows replacement of native  
5 Cys bridges with lactam bridges. Thioether analogs may be readily synthesized using halo-Ala residues commercially available from RSP Amino Acid Analogues.

[0019] The present invention is further directed to derivatives of the above peptides and peptide derivatives which are acyclic permutations in which the cyclic permutants retain the native bridging pattern of native toxin. See, for example, Craik et al. (2001).

10 [0020] The present invention is further directed to a method of treating disorders associated with voltage gated ion channel disorders in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a  $\mu$ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. The present invention is also directed to a pharmaceutical composition comprising a therapeutically effective amount of a  $\mu$ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof and a pharmaceutically acceptable carrier.

15 [0021] More specifically, the present invention is further directed to uses of these peptides or nucleic acids as described herein as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The  $\mu$ -conopeptides are also useful for  
20 treating neuromuscular disorders.

[0022] The present invention is directed to the use of  $\mu$ -conopeptides as a local anesthetic for treating pain. The  $\mu$ -conopeptides have long lasting anesthetic activity and are particularly useful for spinal anesthesia, either administered acutely for post-operative pain or via an intrathecal pump for severe chronic pain situations. The  $\mu$ -conopeptides are also useful as  
25 analgesics in chronic and neuropathic pain states, such as trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain and phantom limb pain. The  $\mu$ -conopeptides are also useful for treating burn pain and as ocular anesthetics.

[0023] The present invention is directed to the use of  $\mu$ -conopeptides as neuroprotectants. The  $\mu$ -conopeptides are useful for the treatment and alleviation of epilepsy  
30 and as a general anticonvulsant agent. The  $\mu$ -conopeptides are also useful for treating neurodegenerative diseases, such as Amyotrophic Lateral Sclerosis (ALS). The  $\mu$ -conopeptides are further useful as cerebroprotectants, such as for reducing neurotoxic injury associated with

conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycemic events.

[0024] The present invention is directed to the use of  $\mu$ -conopeptides as neuromuscular blockers and for treating neuromuscular disorders. As such, the  $\mu$ -conopeptides are useful for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use.

[0025] More specifically, the present invention is also directed to nucleic acids which encode  $\mu$ -conopeptides of the present invention or which encodes precursor peptides for these  $\mu$ -conopeptides, as well as the precursor peptide. The nucleic acid sequences encoding the precursor peptides of other  $\mu$ -conopeptides of the present invention are set forth in Table 1. Table 1 also sets forth the amino acid sequences of these precursor peptides.

[0026] The present invention is further directed to the use of selectively radioiodinated or radiotritiated  $\mu$ -conopeptides for characterizing pore occlusion sites on different sodium channel subtypes or for use in screening assays.

[0027] The present invention is also directed to the use of  $\mu$ -conopeptides for screening small molecule libraries to identify small molecules that are selective blocking agents at specific sodium channel subtypes expressed in mammalian systems. In one embodiment, the blocking activity of a small molecule at a particular sodium channel subtype is compared to the blocking activity of a  $\mu$ -conopeptide at the same sodium channel subtype. In a second embodiment, the ability of a small molecule to displace a  $\mu$ -conopeptide from a sodium channel subtype is determined. In a third embodiment, the binding affinity of a small molecule for a sodium channel subtype is compared to the binding affinity of a  $\mu$ -conopeptide for the same sodium channel subtype.

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

[0028] The present invention is to  $\mu$ -conopeptides, derivatives or pharmaceutically acceptable salts thereof. The present invention is further directed to the use of this peptide, derivatives thereof and pharmaceutically acceptable salts thereof for the treatment of disorders associated with voltage-gated sodium channels. Thus, the  $\mu$ -conopeptides or derivatives are useful as neuromuscular blocking agents, local anesthetic agents, analgesic agents and neuroprotective agents. The  $\mu$ -conopeptides are also useful for treating neuromuscular

disorders. The invention is further directed to nucleic acid sequences encoding the  $\mu$ -conopeptides and encoding propeptides, as well as the propeptides.

[0029] The present invention, in another aspect, relates to a pharmaceutical composition comprising an effective amount of an  $\mu$ -conopeptides, a mutein thereof, an analog thereof, an active fragment thereof or pharmaceutically acceptable salts or solvates. Such a pharmaceutical composition has the capability of acting at voltage gated ion channels, and are thus useful for treating a disorder or disease of a living animal body, including a human, which disorder or disease is responsive to the partial or complete blockade of voltage gated ion channels of the central nervous system comprising the step of administering to such a living animal body, including a human, in need thereof a therapeutically effective amount of a pharmaceutical composition of the present invention.

[0030] The present invention is directed to the use of  $\mu$ -conopeptides as neuromuscular blockers and for treating neuromuscular disorders. As such, the  $\mu$ -conopeptides are useful for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the  $\mu$ -conopeptides are useful as neuromuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the  $\mu$ -conopeptides are useful as agents for treating neuromuscular disorders such as myofacial pain syndrome, chronic muscle spasm, dystonias and spasticity.

[0031] The primary factor detrimental to neurons in neurological disorders associated with deficient oxygen supply or mitochondrial dysfunction is insufficient ATP production relative to their requirement. As a large part of the energy consumed by brain cells is used for maintenance of the  $\text{Na}^+$  gradient across the cellular membrane, reduction of energy demand by down-modulation of voltage-gated  $\text{Na}(+)$ -channels is one strategy for neuroprotection. In addition, preservation of the inward  $\text{Na}^+$  gradient may be beneficial because it is an essential driving force for vital ion exchanges and transport mechanisms such as  $\text{Ca}^{2+}$  homeostasis and neurotransmitter uptake. Thus, the  $\mu$ -conopeptides of the present invention are useful as neuroprotectants.

[0032] Thus, the pharmaceutical compositions of the present invention are useful as neuroprotectants, especially cerebroprotectants, neuromuscular blockers, analgesics (both as a local anesthetic and for general analgesia use) or adjuvants to general anesthetics. A "neurological disorder or disease" is a disorder or disease of the nervous system including, but



not limited to, global and focal ischemic and hemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage as in cardiac arrest or neonatal distress or epilepsy. In addition, a "neurological disorder or disease" is a disease state and condition in which a neuroprotectant, anticonvulsant, analgesic and/or as an adjunct in general anesthesia may be indicated, useful, recommended or prescribed.

[0033] More specifically, the present invention is directed to the use of these compounds for reducing neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, or hypoglycemic events. The present invention is further directed to the use of these compounds for treating pain, including acute and chronic pain, such migraine, nociceptive and neuropathic pain.

[0034] A "neuroprotectant" is a compound capable of preventing the neuronal death associated with a neurological disorder or disease. An "analgesic" is a compound capable of relieving pain by altering perception of nociceptive stimuli without producing anesthesia or loss of consciousness. A "muscle relaxant" is a compound that reduces muscular tension. An "adjunct in general anesthesia" is a compound useful in conjunction with anesthetic agents in producing the loss of ability to perceive pain associated with the loss of consciousness.

[0035] The invention relates as well to methods useful for treatment of neurological disorders and diseases, including, but not limited to, global and focal ischemic and hemorrhagic stroke, head trauma, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy or other convulsive disorders without undesirable side effects.

[0036] Thus, in one embodiment, the invention provides a method of reducing/alleviating/ decreasing the perception of pain by a subject or for inducing analgesia in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a  $\mu$ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. The pain may be acute, persistent, inflammatory or neuropathic pain. The  $\mu$ -conopeptides are useful as an analgesia for chronic and neuropathic pain states, such as trigeminal neuralgia, diabetic neuropathy, post-herpetic neuralgia, neuroma pain, phantom limb pain. These peptides are also useful for treating burn pain and as ocular anesthetics.

[0037] In a second embodiment, the invention provides a method of reducing/alleviating/decreasing the perception of pain by a subject or for inducing analgesia, particularly local analgesia, in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a  $\mu$ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof. These peptides are also useful for treating burn pain and as ocular anesthetics.

[0038] In a third embodiment, the invention provides a method of treating stroke, head or spinal cord trauma or injury, anoxia, hypoxia-induced nerve cell damage, ischemia, migraine, psychosis, anxiety, schizophrenia, inflammation, movement disorder, epilepsy, any other convulsive disorder or in the prevention of the degenerative changes connected with the same in a subject comprising administering to the subject an effective amount of the pharmaceutical composition comprising a therapeutically effective amount of a  $\mu$ -conopeptide described herein or a pharmaceutically acceptable salt or solvate thereof.

[0039] In a fourth embodiment, the invention provides a method for providing a neuromuscular block or for treating neuromuscular disorders, such as methods for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the  $\mu$ -conopeptides are useful as neuromuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the  $\mu$ -conopeptides are useful as agents for treating neuromuscular disorders such as myofascial pain syndrome, chronic muscle spasm, dystonias and spasticity.

[0040] The present invention is also directed to the use of  $\mu$ -conopeptides for screening small molecule libraries to identify small molecules that are selective blocking agents at specific sodium channel subtypes expressed in mammalian systems. In one embodiment, the blocking activity of a small molecule at a particular sodium channel subtype is compared to the blocking activity of a  $\mu$ -conopeptide at the same sodium channel subtype. In a second embodiment, the ability of a small molecule to displace a  $\mu$ -conopeptide from a sodium channel subtype is determined. In a third embodiment, the binding affinity of a small molecule for a sodium channel subtype is compared to the binding affinity of a  $\mu$ -conopeptide for the same sodium channel subtype.

[0041] The  $\mu$ -conopeptides described herein are sufficiently small to be chemically synthesized. General chemical syntheses for preparing the foregoing  $\omega$ -conotoxin peptides are

described hereinafter. Various ones of the  $\mu$ -conopeptides can also be obtained by isolation and purification from specific *Conus* species using the technique described in U.S. Patent Nos. 4,447,356 (Olivera et al., 1984); 5,514,774; 5,719,264; and 5,591,821, as well as in PCT published application WO 98/03189, the disclosures of which are incorporated herein by reference.

[0042] Although the  $\mu$ -conopeptides of the present invention can be obtained by purification from cone snails, because the amounts of  $\mu$ -conopeptides obtainable from individual snails are very small, the desired substantially pure  $\mu$ -conopeptides are best practically obtained in commercially valuable amounts by chemical synthesis using solid-phase strategy. For example, the yield from a single cone snail may be about 10 micrograms or less of  $\mu$ -conopeptides peptide. By "substantially pure" is meant that the peptide is present in the substantial absence of other biological molecules of the same type; it is preferably present in an amount of at least about 85% purity and preferably at least about 95% purity. Chemical synthesis of biologically active  $\mu$ -conopeptides peptides depends of course upon correct determination of the amino acid sequence.

[0043] The  $\mu$ -conopeptides can also be produced by recombinant DNA techniques well known in the art. Such techniques are described by Sambrook et al. (1989). A gene of interest (i.e., a gene that encodes a suitable  $\mu$ -conopeptides) can be inserted into a cloning site of a suitable expression vector by using standard techniques. These techniques are well known to those skilled in the art. The expression vector containing the gene of interest may then be used to transfect the desired cell line. Standard transfection techniques such as calcium phosphate co-precipitation, DEAE-dextran transfection or electroporation may be utilized. A wide variety of host/expression vector combinations may be used to express a gene encoding a conotoxin peptide of interest. Such combinations are well known to a skilled artisan. The peptides produced in this manner are isolated, reduced if necessary, and oxidized to form the correct disulfide bonds.

[0044] One method of forming disulfide bonds in the  $\mu$ -conopeptides of the present invention is the air oxidation of the linear peptides for prolonged periods under cold room temperatures or at room temperature. This procedure results in the creation of a substantial amount of the bioactive, disulfide-linked peptides. The oxidized peptides are fractionated using reverse-phase high performance liquid chromatography (HPLC) or the like, to separate peptides having different linked configurations. Thereafter, either by comparing these fractions with the

elution of the native material or by using a simple assay, the particular fraction having the correct linkage for maximum biological potency is easily determined. However, because of the dilution resulting from the presence of other fractions of less biopotency, a somewhat higher dosage may be required.

5 [0045] The peptides are synthesized by a suitable method, such as by exclusively solid-phase techniques, by partial solid-phase techniques, by fragment condensation or by classical solution couplings.

10 [0046] In conventional solution phase peptide synthesis, the peptide chain can be prepared by a series of coupling reactions in which constituent amino acids are added to the growing peptide chain in the desired sequence. Use of various coupling reagents, e.g., dicyclohexylcarbodiimide or diisopropylcarbonyldimidazole, various active esters, e.g., esters of N-hydroxyphthalimide or N-hydroxy-succinimide, and the various cleavage reagents, to carry out reaction in solution, with subsequent isolation and purification of intermediates, is well known classical peptide methodology. Classical solution synthesis is described in detail in the treatise, "Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden," (1974). Techniques of exclusively solid-phase synthesis are set forth in the textbook, "Solid-Phase Peptide Synthesis," (Stewart and Young, 1969), and are exemplified by the disclosure of U.S. Patent 4,105,603 (Vale et al., 1978). The fragment condensation method of synthesis is exemplified in U.S. Patent 3,972,859 (1976). Other available syntheses are exemplified by U.S. 15 Patents No. 3,842,067 (1974) and 3,862,925 (1975). The synthesis of peptides containing  $\gamma$ -carboxyglutamic acid residues is exemplified by Rivier et al. (1987), Nishiuchi et al. (1993) and Zhou et al. (1996).

20 [0047] Common to such chemical syntheses is the protection of the labile side chain groups of the various amino acid moieties with suitable protecting groups which will prevent a chemical reaction from occurring at that site until the group is ultimately removed. Usually also common is the protection of an  $\alpha$ -amino group on an amino acid or a fragment while that entity reacts at the carboxyl group, followed by the selective removal of the  $\alpha$ -amino protecting group to allow subsequent reaction to take place at that location. Accordingly, it is common that, as a step in such a synthesis, an intermediate compound is produced which includes each of the 25 amino acid residues located in its desired sequence in the peptide chain with appropriate side-chain protecting groups linked to various ones of the residues having labile side chains.

[0048] As far as the selection of a side chain amino protecting group is concerned, generally one is chosen which is not removed during deprotection of the  $\alpha$ -amino groups during the synthesis. However, for some amino acids, e.g., His, protection is not generally necessary. In selecting a particular side chain protecting group to be used in the synthesis of the peptides, the following general rules are followed: (a) the protecting group preferably retains its protecting properties and is not split off under coupling conditions, (b) the protecting group should be stable under the reaction conditions selected for removing the  $\alpha$ -amino protecting group at each step of the synthesis, and (c) the side chain protecting group must be removable, upon the completion of the synthesis containing the desired amino acid sequence, under reaction conditions that will not undesirably alter the peptide chain.

[0049] It should be possible to prepare many, or even all, of these peptides using recombinant DNA technology. However, when peptides are not so prepared, they are preferably prepared using the Merrifield solid-phase synthesis, although other equivalent chemical syntheses known in the art can also be used as previously mentioned. Solid-phase synthesis is commenced from the C-terminus of the peptide by coupling a protected  $\alpha$ -amino acid to a suitable resin. Such a starting material can be prepared by attaching an  $\alpha$ -amino-protected amino acid by an ester linkage to a chloromethylated resin or a hydroxymethyl resin, or by an amide bond to a benzhydrylamine (BHA) resin or paramethylbenzhydrylamine (MBHA) resin. Preparation of the hydroxymethyl resin is described by Bodansky et al. (1966). Chloromethylated resins are commercially available from Bio Rad Laboratories (Richmond, CA) and from Lab. Systems, Inc. The preparation of such a resin is described by Stewart and Young (1969). BHA and MBHA resin supports are commercially available, and are generally used when the desired polypeptide being synthesized has an unsubstituted amide at the C-terminus. Thus, solid resin supports may be any of those known in the art, such as one having the formulae  $-O-CH_2$ -resin support,  $-NH$  BHA resin support, or  $-NH$ -MBHA resin support. When the unsubstituted amide is desired, use of a BHA or MBHA resin is preferred, because cleavage directly gives the amide. In case the N-methyl amide is desired, it can be generated from an N-methyl BHA resin. Should other substituted amides be desired, the teaching of U.S. Patent No. 4,569,967 (Kornreich et al., 1986) can be used, or should still other groups than the free acid be desired at the C-terminus, it may be preferable to synthesize the peptide using classical methods as set forth in the Houben-Weyl text (1974).

[0050] The C-terminal amino acid, protected by Boc or Fmoc and by a side-chain protecting group, if appropriate, can be first coupled to a chloromethylated resin according to the procedure set forth in K. Horiki et al. (1978), using KF in DMF at about 60°C for 24 hours with stirring, when a peptide having free acid at the C-terminus is to be synthesized. Following the coupling of the BOC-protected amino acid to the resin support, the  $\alpha$ -amino protecting group is removed, as by using trifluoroacetic acid (TFA) in methylene chloride or TFA alone. The deprotection is carried out at a temperature between about 0°C and room temperature. Other standard cleaving reagents, such as HCl in dioxane, and conditions for removal of specific  $\alpha$ -amino protecting groups may be used as described in Schroder & Lubke (1965).

[0051] After removal of the  $\alpha$ -amino-protecting group, the remaining  $\alpha$ -amino- and side chain-protected amino acids are coupled step-wise in the desired order to obtain the intermediate compound defined hereinbefore, or as an alternative to adding each amino acid separately in the synthesis, some of them may be coupled to one another prior to addition to the solid phase reactor. Selection of an appropriate coupling reagent is within the skill of the art. Particularly suitable as a coupling reagent is N,N'-dicyclohexylcarbodiimide (DCC, DIC, HBTU, HATU, TBTU in the presence of HoBt or HoAt).

[0052] The activating reagents used in the solid phase synthesis of the peptides are well known in the peptide art. Examples of suitable activating reagents are carbodiimides, such as N,N'-diisopropylcarbodiimide and N-ethyl-N'-(3-dimethylaminopropyl)carbodiimide. Other activating reagents and their use in peptide coupling are described by Schroder & Lubke (1965) and Kapoor (1970).

[0053] Each protected amino acid or amino acid sequence is introduced into the solid-phase reactor in about a twofold or more excess, and the coupling may be carried out in a medium of dimethylformamide (DMF):CH<sub>2</sub>Cl<sub>2</sub> (1:1) or in DMF or CH<sub>2</sub>Cl<sub>2</sub> alone. In cases where intermediate coupling occurs, the coupling procedure is repeated before removal of the  $\alpha$ -amino protecting group prior to the coupling of the next amino acid. The success of the coupling reaction at each stage of the synthesis, if performed manually, is preferably monitored by the ninhydrin reaction, as described by Kaiser et al. (1970). Coupling reactions can be performed automatically, as on a Beckman 990 automatic synthesizer, using a program such as that reported in Rivier et al. (1978).

[0054] After the desired amino acid sequence has been completed, the intermediate peptide can be removed from the resin support by treatment with a reagent, such as liquid

hydrogen fluoride or TFA (if using Fmoc chemistry), which not only cleaves the peptide from the resin but also cleaves all remaining side chain protecting groups and also the  $\alpha$ -amino protecting group at the N-terminus if it was not previously removed to obtain the peptide in the form of the free acid. If Met is present in the sequence, the Boc protecting group is preferably first removed using trifluoroacetic acid (TFA)/ethanedithiol prior to cleaving the peptide from the resin with HF to eliminate potential S-alkylation. When using hydrogen fluoride or TFA for cleaving, one or more scavengers such as anisole, cresol, dimethyl sulfide and methylethyl sulfide are included in the reaction vessel.

[0055] Cyclization of the linear peptide is preferably affected, as opposed to cyclizing the peptide while a part of the peptido-resin, to create bonds between Cys residues. To effect such a disulfide cyclizing linkage, fully protected peptide can be cleaved from a hydroxymethylated resin or a chloromethylated resin support by ammonolysis, as is well known in the art, to yield the fully protected amide intermediate, which is thereafter suitably cyclized and deprotected. Alternatively, deprotection, as well as cleavage of the peptide from the above resins or a benzhydrylamine (BHA) resin or a methylbenzhydrylamine (MBHA), can take place at 0°C with hydrofluoric acid (HF) or TFA, followed by oxidation as described above.

[0056] The peptides are also synthesized using an automatic synthesizer. Amino acids are sequentially coupled to an MBHA Rink resin (typically 100 mg of resin) beginning at the C-terminus using an Advanced Chemtech 357 Automatic Peptide Synthesizer. Couplings are carried out using 1,3-diisopropylcarbodiimide in N-methylpyrrolidinone (NMP) or by 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU) and diethylisopropylethylamine (DIEA). The Fmoc protecting group is removed by treatment with a 20% solution of piperidine in dimethylformamide (DMF). Resins are subsequently washed with DMF (twice), followed by methanol and NMP.

[0057] Muteins, analogs or active fragments, of the foregoing conotoxin peptides are also contemplated here. See, e.g., Hammerland et al. (1992). Derivative muteins, analogs or active fragments of the conotoxin peptides may be synthesized according to known techniques, including conservative amino acid substitutions, such as outlined in U.S. Patent Nos. 5,545,723 (see particularly col. 2, line 50--col. 3, line 8); 5,534,615 (see particularly col. 19, line 45--col. 22, line 33); and 5,364,769 (see particularly col. 4, line 55--col. 7, line 26), each herein incorporated by reference.

[0058] The  $\mu$ -conopeptides of the present invention are also useful to reduce neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal chord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia, or hypoglycemic events. To reduce neurotoxic injury, an  $\omega$ -conopeptide should be administered in a therapeutically effective amount to the patient within 24 hours of the onset of the hypoxic, anoxic or ischemic condition in order for the  $\mu$ -conopeptide to effectively minimize the CNS damage which the patient will experience.

[0059] The  $\mu$ -conopeptides of the present invention are further useful in controlling pain, e.g., as analgesic agents, and the treatment of migraine, acute pain or persistent pain. They can be used prophylactically or to relieve the symptoms associated with a migraine episode, or to treat acute or persistent pain. For these uses, an  $\mu$ -conopeptide is administered in a therapeutically effective amount to overcome or to ease the pain.

[0060] The  $\mu$ -conopeptides of the present invention are also useful as neuromuscular blockers and for treating neuromuscular disorders. They can be used for providing relaxation of muscle, for treating benign essential blepharospasm and other forms of focal dystonia and for anti-wrinkle use. Thus, in one aspect, the  $\mu$ -conopeptides are used as neuromuscular blocking agents in conjunction with surgery or for intubation of the trachea by conventional parenteral administration e.g., intramuscular or intravenous administration in solution. In a second aspect, the  $\mu$ -conopeptides are used as agents for treating neuromuscular disorders such as myofascial pain syndrome, chronic muscle spasm, dystonias and spasticity. For these uses, a  $\mu$ -conopeptide is administered in a therapeutically effective amount to relax muscle or provide a neuromuscular block.

[0061] Pharmaceutical compositions containing a compound of the present invention as the active ingredient can be prepared according to conventional pharmaceutical compounding techniques. See, for example, *Remington's Pharmaceutical Sciences*, 18th Ed. (1990, Mack Publishing Co., Easton, PA). Typically, an antagonistic amount of active ingredient will be admixed with a pharmaceutically acceptable carrier. The carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., intravenous, oral, parenteral or intrathecally. For examples of delivery methods see U.S. Patent No. 5,844,077, incorporated herein by reference.

[0062] "Pharmaceutical composition" means physically discrete coherent portions suitable for medical administration. "Pharmaceutical composition in dosage unit form" means



physically discrete coherent units suitable for medical administration, each containing a daily dose or a multiple (up to four times) or a sub-multiple (down to a fortieth) of a daily dose of the active compound in association with a carrier and/or enclosed within an envelope. Whether the composition contains a daily dose, or for example, a half, a third or a quarter of a daily dose, will depend on whether the pharmaceutical composition is to be administered once or, for example, twice, three times or four times a day, respectively.

[0063] The term "salt", as used herein, denotes acidic and/or basic salts, formed with inorganic or organic acids and/or bases, preferably basic salts. While pharmaceutically acceptable salts are preferred, particularly when employing the compounds of the invention as medicaments, other salts find utility, for example, in processing these compounds, or where non-medicament-type uses are contemplated. Salts of these compounds may be prepared by art-recognized techniques.

[0064] Examples of such pharmaceutically acceptable salts include, but are not limited to, inorganic and organic addition salts, such as hydrochloride, sulphates, nitrates or phosphates and acetates, trifluoroacetates, propionates, succinates, benzoates, citrates, tartrates, fumarates, maleates, methane-sulfonates, isothionates, theophylline acetates, salicylates, respectively, or the like. Lower alkyl quaternary ammonium salts and the like are suitable, as well.

[0065] As used herein, the term "pharmaceutically acceptable" carrier means a non-toxic, inert solid, semi-solid liquid filler, diluent, encapsulating material, formulation auxiliary of any type, or simply a sterile aqueous medium, such as saline. Some examples of the materials that can serve as pharmaceutically acceptable carriers are sugars, such as lactose, glucose and sucrose, starches such as corn starch and potato starch, cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt, gelatin, talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol, polyols such as glycerin, sorbitol, mannitol and polyethylene glycol; esters such as ethyl oleate and ethyl laurate, agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline, Ringer's solution; ethyl alcohol and phosphate buffer solutions, as well as other non-toxic compatible substances used in pharmaceutical formulations.

[0066] Wetting agents, emulsifiers and lubricants such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening,

flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator. Examples of pharmaceutically acceptable antioxidants include, but are not limited to, water soluble antioxidants such as ascorbic acid, cysteine hydrochloride, sodium bisulfite, sodium metabisulfite, sodium sulfite, and the like; oil soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, aloha-tocopherol and the like; and the metal chelating agents such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid and the like.

[0067] For oral administration, the compounds can be formulated into solid or liquid preparations such as capsules, pills, tablets, lozenges, melts, powders, suspensions or emulsions.

In preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed, such as, for example, water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents, suspending agents, and the like in the case of oral liquid preparations (such as, for example, suspensions, elixirs and solutions); or carriers such as starches, sugars, diluents, granulating agents, lubricants, binders, disintegrating agents and the like in the case of oral solid preparations (such as, for example, powders, capsules and tablets). Because of their ease in administration, tablets and capsules represent the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. If desired, tablets may be sugar-coated or enteric-coated by standard techniques. The active agent can be encapsulated to make it stable to passage through the gastrointestinal tract while at the same time allowing for passage across the blood brain barrier. See for example, WO 96/11698.

[0068] For parenteral administration, the compound may be dissolved in a pharmaceutical carrier and administered as either a solution or a suspension. Illustrative of suitable carriers are water, saline, dextrose solutions, fructose solutions, ethanol, or oils of animal, vegetative or synthetic origin. The carrier may also contain other ingredients, for example, preservatives, suspending agents, solubilizing agents, buffers and the like. When the compounds are being administered intrathecally, they may also be dissolved in cerebrospinal fluid.

[0069] A variety of administration routes are available. The particular mode selected will depend of course, upon the particular drug selected, the severity of the disease state being treated and the dosage required for therapeutic efficacy. The methods of this invention, generally speaking, may be practiced using any mode of administration that is medically acceptable,

meaning any mode that produces effective levels of the active compounds without causing clinically unacceptable adverse effects. Such modes of administration include oral, rectal, sublingual, topical, nasal, transdermal or parenteral routes. The term "parenteral" includes subcutaneous, intravenous, epidural, irrigation, intramuscular, release pumps, or infusion.

5 [0070] For example, administration of the active agent according to this invention may be achieved using any suitable delivery means, including:

(a) pump (see, e.g., Luer & Hatton (1993), Zimm et al. (1984) and Ettinger et al. (1978));

(b), microencapsulation (see, e.g., U.S. Patent Nos. 4,352,883; 4,353,888; and 5,084,350);

10 (c) continuous release polymer implants (see, e.g., U.S. Patent No. 4,883,666);

(d) macroencapsulation (see, e.g., U.S. Patent Nos. 5,284,761, 5,158,881, 4,976,859 and 4,968,733 and published PCT patent applications WO92/19195, WO 95/05452);

(e) naked or unencapsulated cell grafts to the CNS (see, e.g., U.S. Patent Nos. 5,082,670 and 5,618,531);

15 (f) injection, either subcutaneously, intravenously, intra-arterially, intramuscularly, or to other suitable site; or

(g) oral administration, in capsule, liquid, tablet, pill, or prolonged release formulation.

[0071] In one embodiment of this invention, an active agent is delivered directly into the CNS, preferably to the brain ventricles, brain parenchyma, the intrathecal space or other suitable  
20 CNS location, most preferably intrathecally.

[0072] Alternatively, targeting therapies may be used to deliver the active agent more specifically to certain types of cell, by the use of targeting systems such as antibodies or cell specific ligands. Targeting may be desirable for a variety of reasons, e.g. if the agent is unacceptably toxic, or if it would otherwise require too high a dosage, or if it would not  
25 otherwise be able to enter the target cells.

[0073] The active agents, which are peptides, can also be administered in a cell based delivery system in which a DNA sequence encoding an active agent is introduced into cells designed for implantation in the body of the patient, especially in the spinal cord region. Suitable delivery systems are described in U.S. Patent No. 5,550,050 and published PCT  
30 Application Nos. WO 92/19195, WO 94/25503, WO 95/01203, WO 95/05452, WO 96/02286, WO 96/02646, WO 96/40871, WO 96/40959 and WO 97/12635. Suitable DNA sequences can

be prepared synthetically for each active agent on the basis of the developed sequences and the known genetic code.

[0074] Exemplary methods for administering such muscle relaxant compounds (e.g., so as to achieve sterile or aseptic conditions) will be apparent to the skilled artisan. Certain methods suitable for administering compounds useful according to the present invention are set forth in Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, 7th Ed. (1985). The administration to the patient can be intermittent; or at a gradual, continuous, constant or controlled rate. Administration can be to a warm-blooded animal (e.g. a mammal, such as a mouse, rat, cat, rabbit, dog, pig, cow or monkey); but advantageously is administered to a human being. Administration occurs after general anesthesia is administered. The frequency of administration normally is determined by an anesthesiologist, and typically varies from patient to patient.

[0075] The active agent is preferably administered in an therapeutically effective amount. By a "therapeutically effective amount" or simply "effective amount" of an active compound is meant a sufficient amount of the compound to treat the desired condition at a reasonable benefit/risk ratio applicable to any medical treatment. The actual amount administered, and the rate and time-course of administration, will depend on the nature and severity of the condition being treated. Prescription of treatment, e.g. decisions on dosage, timing, etc., is within the responsibility of general practitioners or specialists, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of techniques and protocols can be found in *Remington's Pharmaceutical Sciences*.

[0076] Dosage may be adjusted appropriately to achieve desired drug levels, locally or systemically. Typically the active agents of the present invention exhibit their effect at a dosage range from about 0.001 mg/kg to about 250 mg/kg, preferably from about 0.01 mg/kg to about 100 mg/kg of the active ingredient, more preferably from about 0.05 mg/kg to about 75 mg/kg. A suitable dose can be administered in multiple sub-doses per day. Typically, a dose or sub-dose may contain from about 0.1 mg to about 500 mg of the active ingredient per unit dosage form. A more preferred dosage will contain from about 0.5 mg to about 100 mg of active ingredient per unit dosage form. Dosages are generally initiated at lower levels and increased until desired effects are achieved. In the event that the response in a subject is insufficient at such doses, even higher doses (or effective higher doses by a different, more localized delivery

route) may be employed to the extent that patient tolerance permits. Continuous dosing over, for example 24 hours or multiple doses per day are contemplated to achieve appropriate systemic levels of compounds.

[0077] For the treatment of pain, if the route of administration is directly to the CNS, the dosage contemplated is from about 1 ng to about 100 mg per day, preferably from about 100 ng to about 10 mg per day, more preferably from about 1  $\mu$ g to about 100  $\mu$ g per day. If administered peripherally, the dosage contemplated is somewhat higher, from about 100 ng to about 1000 mg per day, preferably from about 10  $\mu$ g to about 100 mg per day, more preferably from about 100  $\mu$ g to about 10 mg per day. If the conopeptide is delivered by continuous infusion (e.g., by pump delivery, biodegradable polymer delivery or cell-based delivery), then a lower dosage is contemplated than for bolus delivery.

[0078] Advantageously, the compositions are formulated as dosage units, each unit being adapted to supply a fixed dose of active ingredients. Tablets, coated tablets, capsules, ampoules and suppositories are examples of dosage forms according to the invention.

[0079] It is only necessary that the active ingredient constitute an effective amount, i.e., such that a suitable effective dosage will be consistent with the dosage form employed in single or multiple unit doses. The exact individual dosages, as well as daily dosages, are determined according to standard medical principles under the direction of a physician or veterinarian for use humans or animals.

[0080] The pharmaceutical compositions will generally contain from about 0.0001 to 99 wt. %, preferably about 0.001 to 50 wt. %, more preferably about 0.01 to 10 wt.% of the active ingredient by weight of the total composition. In addition to the active agent, the pharmaceutical compositions and medicaments can also contain other pharmaceutically active compounds. Examples of other pharmaceutically active compounds include, but are not limited to, analgesic agents, cytokines and therapeutic agents in all of the major areas of clinical medicine. When used with other pharmaceutically active compounds, the conopeptides of the present invention may be delivered in the form of drug cocktails. A cocktail is a mixture of any one of the compounds useful with this invention with another drug or agent. In this embodiment, a common administration vehicle (e.g., pill, tablet, implant, pump, injectable solution, etc.) would contain both the instant composition in combination supplementary potentiating agent. The individual drugs of the cocktail are each administered in therapeutically effective amounts. A therapeutically effective amount will be determined by the parameters described above; but, in

any event, is that amount which establishes a level of the drugs in the area of body where the drugs are required for a period of time which is effective in attaining the desired effects.

[0081] The practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, genetics, immunology, cell biology, cell culture and transgenic biology, which are within the skill of the art. See, e.g., Maniatis *et al.*, 1982; Sambrook *et al.*, 1989; Ausubel *et al.*, 1992; Glover, 1985; Anand, 1992; Guthrie and Fink, 1991; Harlow and Lane, 1988; Jakoby and Pastan, 1979; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Riott, *Essential Immunology*, 6th Edition, Blackwell Scientific Publications, Oxford, 1988; Hogan et al., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

### EXAMPLES

[0082] The present invention is described by reference to the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below were utilized.

#### EXAMPLE 1

##### Isolation of $\mu$ -Conopeptides

[0083] Crude venom was extracted from venom ducts (Cruz et al., 1976), and the components were purified as previously described (Cartier et al., 1996). The crude extract from venom ducts was purified by reverse phase liquid chromatography (RPLC) using a Vydac C<sub>18</sub>

semi-preparative column (10 x 250 mm). Further purification of bioactive peaks was done on a Vydac C<sub>18</sub> analytical column (4.6 x 220 mm). The effluents were monitored at 220 nm. Peaks were collected, and aliquots were assayed for activity. Throughout purification, HPLC fractions were assayed by means of intracerebral ventricular (i.c.v.) injection into mice (Clark et al., 1981).

[0084] The amino acid sequence of the purified peptides were determined by standard methods. The purified peptides were reduced and alkylated prior to sequencing by automated Edman degradation on an Applied Biosystems 477A Protein Sequencer with a 120A Analyzer (DNA/Peptide Facility, University of Utah) (Martinez et al., 1995; Shon et al., 1994).

[0085] In accordance with this method, the  $\mu$ -conopeptides described as "isolated" in Table 1 were obtained. These  $\mu$ -conopeptides, as well as the other  $\mu$ -conopeptides and the  $\mu$ -conopeptide precursors set forth in Table 1 are synthesized as described in U.S. Patent No. 5,670,622.

## EXAMPLE 2

### Isolation of DNA Encoding $\mu$ -Conopeptides

[0086] DNA coding for  $\mu$ -conopeptides was isolated and cloned in accordance with conventional techniques using general procedures well known in the art, such as described in Olivera et al. (1996). Alternatively, cDNA libraries was prepared from *Conus* venom duct using conventional techniques. DNA from single clones was amplified by conventional techniques using primers which correspond approximately to the M13 universal priming site and the M13 reverse universal priming site. Clones having a size of approximately 300-500 nucleotides were sequenced and screened for similarity in sequence to known  $\mu$ -conotoxins. The DNA sequences and encoded propeptide sequences are set forth in Table 1. DNA sequences coding for the mature toxin can also be prepared on the basis of the DNA sequences set forth in Table 1. An alignment of the  $\mu$ -conopeptides of the present invention is set forth in Table 2.

TABLE 1

DNA and Amino Acid Sequences of  $\mu$ -Conopeptides and Precursors

<b>Name:</b>	Ar3.1
<b>Species:</b>	arenatus
<b>Cloned:</b>	Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTCTTGACCATCTG  
 TATGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGGATGGGGATCAACCTGCAGACCG  
 ACCTGCAGAGCGTATGCAGGACGACTTTATAACTGAGCATCATCCCCTGTTTGATCC  
 5 TGTCAAACGGTGTGCGAGAGGCCATGCAACATAGGATGCGTACCTTGTTGTTAATG  
 ACCAGCTTTGTCATCGCGGCCTCATCAAGCGAATAAGTAAAACGATTGCAGT (SEQ  
 ID NO:1)

**Translation:**

10 MMSKLGVFLTICMLLFPLTALPLDGDQPADRPAERMQDDFITEHHPLFDPVKRCCERPC  
 NIGCVPC (SEQ ID NO:2)

**Toxin Sequence:**

Cys-Cys-Xaa1-Arg-Xaa3-Cys-Asn-Ile-Gly-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:3)

15  
**Name:** Ak3.1  
**Species:** atlanticus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAC  
 TTACTGCTCTTCCGCTGGATGAAGATCAACCGGTACACCGACCTGCAGAGCGTATGC  
 AGGACATTTTCATCTGATCAACATCTCTTCTTTGATCTCATCAAACGGTGCTGCGAGT  
 20 TGCCATGCGGGGCCAGGCTTTTGCCTCCCTTGTTGCTGACATCAATAACGTGTTGATG  
 ACCAACTTTCTCGAG (SEQ ID NO:4)

**Translation:**

30 GSMMSKLGVLLTICLLLFPLTALPLDEDQPVHRPAERMQDISSDQHLFFDLIKRCCELPC  
 GPGFCVPCC (SEQ ID NO:5)

**Toxin Sequence:**

Cys-Cys-Xaa1-Leu-Xaa3-Cys-Gly-Xaa3-Gly-Phe-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:6)

35  
**Name:** A3.1  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

40 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
 TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGTAGACCGA  
 CCTGAAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGCATCCCTTGTTTAATCAG  
 AAAAGAATGTGTTGCGGCGAAGGCCGGAATGCCCCAGCTATTTTCAGAAACAGTCA  
 45 GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACT  
 AATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:7)



**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPEERMQDDISSEQHPLFNQKRMCCGEG  
RKCPYSYFRNSQICHCC (SEQ ID NO:8)

5 **Toxin Sequence:**

Met-Cys-Cys-Gly-Xaa1-Gly-Arg-Lys-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-  
Cys-Cys-^ (SEQ ID NO:9)

10 **Name:** A3.2  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

15 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTTTGCTTCTGTTTCCCC  
TTACTGCTCTTCCGATCGATGGAGATCAATCTGTAGACCGACCTGCAGAGCGTATGC  
AGGATGACATTTTCATCTGAGCAGCATCGCTTGTTCAATCAGAAAAGAAGGTGCTGC  
CGGTGGCCATGCCCCCGACAAATCGACGGTGAATATTGTGGCTGTTGCCTTGGATGA  
TAACCGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:10)

**Translation:**

GSMMSKLGVLLTICLLLFPLTALPIDGDQSVDRPAERMQDDISSEQHRLFNQKRRCRW  
PCPRQIDGEYCGCCLG (SEQ ID NO:11)

**Toxin Sequence:**

Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Arg-Gln-Ile-Asp-Gly-Xaa1-Xaa5-Cys-Gly-Cys-Cys-Leu-#  
(SEQ ID NO:12)

30 **Name:** A3.3  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

35 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC  
TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC  
AGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA  
CTGGGAAGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT  
GGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:13)

40

**Translation:**

GSMMSKLGVLLTICLLLFPLTAFPMMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCT  
GKKGSCSGKACKNLKCCSGR (SEQ ID NO:14)

45 **Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-  
Cys-Cys-Ser-# (SEQ ID NO:15)

**Name:** A3.4  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTGTCTGCTTCTGTTTCCAC  
 TTAGTGCTGTTCCGCTGGATGGAGATCAACCTCTAGACCGACACGCGGAGCGTATGC  
 ATGATGGCATTTCACCTAAACGCCATCCCTGGTTTGATCCCGTCAAACGGTGTTGCA  
 AGGTGCAATGCGAGTCTTGACCCCTTGTTGCTAACGTGTTGATGACCAACTTTCTC  
 GAG (SEQ ID NO:16)

**Translation:**

GSMMSKLGVLLTICLLFPLTAVPLDGDQPLDRHAERMHDGISPKRHPWFDPVKRCKK  
 VQCESCTPCC (SEQ ID NO:17)

**Toxin Sequence:**

Cys-Cys-Lys-Val-Gln-Cys-Xaa1-Ser-Cys-Thr-Xaa3-Cys-Cys-^ (SEQ ID NO:18)

**Name:** Bn3.1  
**Species:** bandanus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTATGCTTCTGTTTCCCC  
 TCACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAGT  
 CAGGACGTTTCATCTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGTTGCAAC  
 TGGCCATGCTCCATGGGATGCATCCCTTGTTGCTACTATTAATAACGTGTTGATGAC  
 CAACTTTCTCGAG (SEQ ID NO:19)

**Translation:**

GSMMSKLGVLLTICMLLFPLTALPMDGDQPADRPAERSQDVSSEQHPLFDPVKRCCNW  
 PCSMGCIPCCYY (SEQ ID NO:20)

**Toxin Sequence:**

Cys-Cys-Asn-Xaa4-Xaa3-Cys-Ser-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Xaa5-Xaa5-^ (SEQ ID NO:21)

**Name:** Bt3.1  
**Species:** betulinus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTCTG

TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG  
 ACCTGCAGAGCGTATGCAGGACATTTTCATCTGAACAGCATCCCTTGTTTGATCCCGT  
 CAAACGGTGTTGCGAATTGCCATGCCATGGATGCGTCCCTTGTTGCTGGCCTTAATA  
 ACGTGTGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATAAGT  
 5 AAAATGATTGCAGT (SEQ ID NO:22)

**Translation:**

MMSKLGVLLTFCLLLFPLTALPLDEDQPADRPAERMQDISSEQHPLFDPVKRCCELPCH  
 GCVPCCPW (SEQ ID NO:23)

**Toxin Sequence:**

Cys-Cys-Xaa1-Leu-Xaa3-Cys-His-Gly-Cys-Val-Xaa3-Cys-Cys-Xaa4-Xaa3-^ (SEQ ID NO:24)

**Name:** Bt3.2  
**Species:** betulinus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTCTG  
 TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG  
 ACATGCAGAGCGTATGCAGGACATTTACCTGAACAGCATCCCTCGTTTGATCCCGT  
 CAAACGGTGTTGCGGGCTGCCATGCAATGGATGCGTCCCTTGTTGCTGGCCTTCATA  
 ACGTGTGGACGACCAACTTTGTTATCACGGCCACGTCAAGTGTCTGATGAATAAGTA  
 AAACGATTGCAGT (SEQ ID NO:25)

**Translation:**

MMSKLGVLLTFCLLLFPLTALPLDEDQPADRHAERMQDISPEQHPSFDPVKRCCGLPCN  
 GCVPCCPWS (SEQ ID NO:26)

**Toxin Sequence:**

Cys-Cys-Gly-Leu-Xaa3-Cys-Asn-Gly-Cys-Val-Xaa3-Cys-Cys-Xaa4-Xaa3-Ser-^ (SEQ ID NO:27)

**Name:** Bt3.3  
**Species:** betulinus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGTTGACCATCTA  
 TATGCTTCTGTTTCCCTTTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCAA  
 CCTCTAGAGCGCATGCAGTATGACATGTTACGTGCAGTGAATCCCTGGTTTGATCCC  
 GTCAAAAGGTGCTGCTCGAGGAACTGCGCAGTATGCATCCCTTGTTGCCCGAATTGG  
 CCAGCTTGATTATCGCGGCCAAGAGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:28)

**Translation:**

MMFKLGVLLTIYMLLPFTALPLDGDQPADQPLERMQYDMLRAVNPWFDPVKRCCSR  
NCAVCIPCCPNWPA (SEQ ID NO:29)

5

**Toxin Sequence:**

Cys-Cys-Ser-Arg-Asn-Cys-Ala-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-Xaa4-Xaa3-Ala-^ (SEQ  
ID NO:30)

10

**Name:** Bu3.1  
**Species:** bullatus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTTTGGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA  
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGAATTCCTTGCTTGAGAA  
GAGAGTTACTGACAGGTGCTGCAAAGGGAAGAGGGAATGCGGCAGATGGTGCAGA  
GATCACTCGCGTTGTTGCGGTCGACGATAAGCTGTTGATGACCAGCTTTGTTATCAC  
GGCTACATCAAGTGTCTAGTGAATAAGTAAAATGATTGCAGT (SEQ ID NO:31)

**Translation:**

MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSEQNSLLEKRVTDRCCCKG  
KRECGRWCRDHSRCCGRR (SEQ ID NO:32)

**Toxin Sequence:**

Val-Thr-Asp-Arg-Cys-Cys-Lys-Gly-Lys-Arg-Xaa1-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-  
Arg-Cys-Cys-# (SEQ ID NO:33)

30

**Name:** Bu3.1A  
**Species:** bullatus  
**Cloned:** Yes

35

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTTTGGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA  
CCTGCAGAGCGTATGCAGGATGACATTTTCATCTGAGCAGAATCCCTTGCTTGAGAA  
GAGAGTTGGTGACAGGTGCTGCAAAGGGAAGAGGGGGTGCAGGAGATGGTGCAGA  
GATCACTCACGTTGTTGCGGTCGACGATAACGTGTTGATGACCAGCTTTGTTATCAC  
GGCTACATCAAGTGTCTTAGTGATTAAGTAAACGATTGCAGT (SEQ ID NO:34)

40

**Translation:**

MMSKLGVLLTICLLLFPLFALRQDGDQPADRPAERMQDDISSEQNPLLEKRVGDRCCCK  
GKRGCGRWCRDHSRCCGRR (SEQ ID NO:35)

45

**Toxin Sequence:**

Val-Gly-Asp-Arg-Cys-Cys-Lys-Gly-Lys-Arg-Gly-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:36)

5

**Name:** Bu3.2  
**Species:** bullatus  
**Cloned:** Yes

10 **DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
 TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA  
 CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGAATCCCTTGCTTGAGAA  
 GAGAGTTGGTGAAAGGTGCTGCAAAAACGGGAAGAGGGGGTGCGGCAGATGGTGC  
 AGAGATCACTCACGTTGTTGCGGTCGACGATAACGTGTTGATGACCGAGGCTTTCGT  
 TATCACGGCTACATCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID  
 NO:37)

**Translation:**

MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSEQNPLLEKRVGERCCKN  
 GKRGCGRWCRDHSRCCGRR (SEQ ID NO:38)

**Toxin Sequence:**

Val-Gly-Xaa1-Arg-Cys-Cys-Lys-Asn-Gly-Lys-Arg-Gly-Cys-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:39)

**Name:** Bu3.3  
**Species:** bullatus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
 TCTGCTTCTGTTTCCCCTTTTTGCTCTTCCGCAGGACGGAGATCAACCTGCAGACCG  
 ACCTGCAGAGCGTATGCAGGACGACCTTTTCATCTGAGCAGCATCCCTTGTTTGAGAA  
 GAGAATTGTTGACAGGTGCTGCAACAAAGGGAACGGGAAGAGGGGGTGACGAGCAGA  
 TGGTGCAGAGATCACTCACGTTGTTGCGGTCGACGATGAACTGTTGATGACCGAGG  
 CTTTGTTATCACGGCTACATCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT  
 (SEQ ID NO:40)

**Translation:**

MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDLSEQHPLFEKRIVDRCCNK  
 GNGKRGCSRWCRDHSRCCGRR (SEQ ID NO:41)

**Toxin Sequence:**

Ile-Val-Asp-Arg-Cys-Cys-Asn-Lys-Gly-Asn-Gly-Lys-Arg-Gly-Cys-Ser-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-Cys-Cys-# (SEQ ID NO:42)

**Name:** Bu3.4  
**Species:** bullatus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTTTGGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA  
CCTGCTGAGCGTATGCAGGACGACATTTTCATCTGAGCGGAATCCCTTGTTTGAGAAG  
AGCGTTGGTTTATATTGCTGCCGACCCAAACCCAACGGGCAGATGATGTGCGACAG  
ATGGTGCGAAAAAACTCACGTTGTTGCGGTCGACGATAATGTGTTGATGACCAGC  
TTTGTTATCAAGGCTACATCAAGTATCTAGTGAATAAGTAAAACGATTGCAGT (SEQ  
ID NO:43)

**Translation:**

MMSKLGVLLTICLLLFPLFALPQDGDQPADRPAERMQDDISSERNPLFEKSVGLYCCRP  
KPNGQMMCDRWCEKNSRCCGRR (SEQ ID NO:44)

**Toxin Sequence:**

Val-Gly-Leu-Xaa5-Cys-Cys-Arg-Xaa3-Lys-Xaa3-Asn-Gly-Gln-Met-Met-Cys-Asp-Arg-Xaa4-  
Cys-Xaa1-Lys-Asn-Ser-Arg-Cys-Cys-# (SEQ ID NO:45)

-----  
**Name:** Bu3.5  
**Species:** bullatus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTTTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGTAGACCGA  
CCTGCAGAACGTATGCAGGACGACCTTTTCATCTGAGCAGCATCCCTTGTTTGTTTTCAG  
AAAAGAAGGTGTTGCGGCGAAGGCTTGACATGCCCCAGATATTGGAAAAACAGTCA  
GATTTGTGCTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGGTATCACGACT  
ACGCCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:46)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPAERMQDDLSEQHPLFVQKRRCCGEG  
LTCPRYWKNSQICACC (SEQ ID NO:47)

**Toxin Sequence:**

Arg-Cys-Cys-Gly-Xaa1-Gly-Leu-Thr-Cys-Xaa3-Arg-Xaa5-Xaa4-Lys-Asn-Ser-Gln-Ile-Cys-Ala-  
Cys-Cys-^ (SEQ ID NO:48)

**Name:** Bu3.5A  
**Species:** bullatus  
**Cloned:** Yes

5 **DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTTTGGCTCTTCCGCAGGATGGAGATCAACCTGCAGACCGA  
CCTGCTGAGCGTATGCAGGACGACATTTTCATCTGAGCAGGATCCCTTGTTTGTTTCAG  
AAAAGAAGGTGTTGCGGCGAAGGCTTGACATGCCCCAGATATTGGAAAAACAGTCA  
10 GATTTGTGCTTGTTGTTAAATGACAACGTGTGATGACCAACTTCGGTATCACGACTA  
CGCCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:49)

**Translation:**

MMSKLGVLITICLLLFPLFALPQDGDQPADRP AERMQDDISSEQDPLFVQKRRCCGEG  
15 TCPRYWKNSQICACC (SEQ ID NO:50)

**Toxin Sequence:**

Arg-Cys-Cys-Gly-Xaa1-Gly-Leu-Thr-Cys-Xaa3-Arg-Xaa5-Xaa4-Lys-Asn-Ser-Gln-Ile-Cys-Ala-  
20 Cys-Cys-^ (SEQ ID NO:51)

**Name:** Cp3.1  
**Species:** capitaneus  
**Cloned:** Yes

25 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGGTGACCATCTGCCTGCTTCTGTTTCCC  
CTTGCTGCTTTTCCACTGGATGGAAATCAACCTGCAGACCACCCTGCAAAGCGTACG  
CAAGATGACAGTTCAGCTGCCCTGATCAATACCTGGATTGATCATTCCCATTCTTGC  
30 TGCAGGGACTGCGGTGAAGATTGTGTTGGTTGTTGCCGGTAACGTGTTGATGACCAA  
CTTTCTCGAG (SEQ ID NO:52)

**Translation:**

GSMMSKLGVLVTICLLLFPLAAFPLDGNQPADHPAKRTQDDSSAALINTWIDHSHSCCR  
35 DCGEDCVGCCCR (SEQ ID NO:53)

**Toxin Sequence:**

Ser-Cys-Cys-Arg-Asp-Cys-Gly-Xaa1-Asp-Cys-Val-Gly-Cys-Cys-Arg-^ (SEQ ID NO:54)

40 **Name:** Ca3.1  
**Species:** characteristicus  
**Cloned:** Yes

45 **DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA

ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAT  
GAGAAAAAGGTGTTGCGGCCCCGGCGGTTTCATGCCCCGTATATTTTCAGAGACAATT  
TTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGAC  
TACGCCAAGTGTCTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:55)

5

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDMRKRCCGPG  
GSCPVYFRDNFICGCC (SEQ ID NO:56)

10

**Toxin Sequence:**

Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-Cys-Gly-Cys-  
Cys-^ (SEQ ID NO:57)

15

**Name:** Ca3.2  
**Species:** characteristic  
**Cloned:** Yes

20

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCTGCAAACCG  
ACCTGTCGAGCGTATGCAGGACAACATTTTCATCTGAGCAGTATCCCTTGTTTGAGAA  
GAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAGACCGACAATGCAAACCCC  
AGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACGGCTACGTCA  
AGTGTTTAGTGAATAAGTAAAATGATTGCAGT (SEQ ID NO:58)

25

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK  
KCKDRQCKPQRCCAGR (SEQ ID NO:59)

30

**Toxin Sequence:**

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-  
Cys-Cys-Ala-# (SEQ ID NO:60)

35

**Name:** Ca3.3  
**Species:** characteristic  
**Cloned:** Yes

40

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCACTGGATGGAGATCAACCTGCAGATCAA  
TCTGCAGAGCGACCTGCAGAGCGTACGCAGGACGACATTCAGCAGCATCCGTTATA  
TGATCCGAAAAGAAGGTGTTGCCGTTATCCATGCCCCGACAGCTGCCACGGATCTTG  
CTGCTATAAGTGATAACATGTTGATGGCCAGCTTTGTTATCACGGCCACGTCAAGTG  
TCTTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:61)

45



**Translation:**

MMSKLGVLITICLLLFPLTALPLDGDQPADQSAERPAERTQDDIQQHPLYDPKRRCCRY  
PCPDSCHGSCCYK (SEQ ID NO:62)

5 **Toxin Sequence:**

Arg-Cys-Cys-Arg-Xaa5-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Gly-Ser-Cys-Cys-Xaa5-Lys-^ (SEQ  
ID NO:63)

10 **Name:** Ca3.4  
**Species:** characteristicus  
**Cloned:** Yes

**DNA Sequence:**

15 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
AACCTGCACAGCGTCTGCAGGACCGCATTCCAACCTGAAGATCATCCCTTATTTGATC  
CCAACAAACGGTGTGCCCCGCCGGTGGCATGCAACATGGGATGCAAGCCTTGTTGT  
20 GGATGACCAGCTTTGTTATCGCGGTCTTCATGAAGTGTCTTAATGAATAAGTAAAAT  
GATTGCAGT (SEQ ID NO:64)

**Translation:**

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAQRLQDRIPTEDHPLFDPNKRCCPPVA  
CNMGCKPCCG (SEQ ID NO:65)

**Toxin Sequence:**

Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:66)

30 **Name:** Ca3.5  
**Species:** characteristicus  
**Cloned:** Yes

**DNA Sequence:**

35 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
AACCTGCAGAGCGTCTGCATGACCGCCFTCCAACCTGAAAATCATCCCTTATATGATC  
CCGTCAAACGGTGTGCGATGATTGCGAATGCGACTATTCTTGCTGGCCTTGCTGTA  
40 TGTTTGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAC  
GATTGCAGT (SEQ ID NO:67)

**Translation:**

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLHDRLPTENHPLYDPVKRCCDDSE  
CDYSCWPCCMFG (SEQ ID NO:68)

45 **Toxin Sequence:**

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Met-Phe-# (SEQ ID

NO:69)

**Name:** Ca3.6  
**Species:** characteristic  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTA CTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAAG  
 CAGGACGTTTCATCTGAACAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCCGC  
 CGGTGTTACATGGGATGCATCCCTTGTTGCTTTTAACGTGTTGATGACCAACTTTCTC  
 GAG (SEQ ID NO:70)

**Translation:**

GSMMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERKQDVSSEQHPFFDPVKRCCRRC  
 YMGCI PCCF (SEQ ID NO:71)

**Toxin Sequence:**

Cys-Cys-Arg-Arg-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:72)

**Name:** Cr3.1  
**Species:** circumcisis  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGGGTATTGTTGACCATCT  
 GTCTGCTTCTGTTTCCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACC  
 AACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATA  
 AGAGACGAAAGTGTTGCGGCAAAGACGGGCCATGCCCCAAATATTTCAAAGACAAT  
 TTTATTTGTGGTTGTTGTTAAATGACAACGTGTTCGATGACCAACTTCGTTATCACGAT  
 TCGCCAAGTGTCTTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:73)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRRKCCGKD  
 GPCPKYFKDNFICGCC (SEQ ID NO:74)

**Toxin Sequence:**

Arg-Lys-Cys-Cys-Gly-Lys-Asp-Gly-Xaa3-Cys-Xaa3-Lys-Xaa5-Phe-Lys-Asp-Asn-Phe-Ile-Cys-  
 Gly-Cys-Cys-^ (SEQ ID NO:75)

**Name:** Da3.1  
**Species:** dalli  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
 GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
 AACCTGCAGAGCGTCTGCAGGACCGCCTTCCAAGTCAAATCATCCCTTATATGATC  
 5 CCGTCAAACGGTGTTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTA  
 TTTTATCATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAAT  
 GATTGCAGT (SEQ ID NO:76)

**Translation:**

10 MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCDDSE  
 CDYSCWPCCILS (SEQ ID NO:77)

**Toxin Sequence:**

15 Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Leu-Ser-^ (SEQ  
 ID NO:78)

**Name:** Da3.2

**Species:** dalli

**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATTG  
 TCTACTTCTGTTTTCCCTTACTGCTGTTCCACTGGATGGAGATCAGCCTGCAGACCG  
 20 ACCTGCAGAGCGTATGCAGGACGGCATTTCATCTGAACATCATCCATTTTTTTGATTG  
 CGTCAAAAAGAAACAACAGTGTTGCCCGCCGGTGGCATGCAACATGGGATGCGAGC  
 CTTGTTGTGGATGACCAGCTTTGTTATCGCGGCTCATGAAGTGTCTAATGAATAAG  
 TAAAACGATTGCAGT (SEQ ID NO:79)

**Translation:**

30 MMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDGISSEHHPFFDSVKKKQQCCP  
 PVACNMGCEPCCG (SEQ ID NO:80)

**Toxin Sequence:**

35 Xaa2-Gln-Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Xaa1-Xaa3-Cys-Cys-# (SEQ  
 ID NO:81)

**Name:** Da3.3

40 **Species:** dalli

**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATATG  
 45 TCTATTTCTGTTTTCCCTTACTGCTGTTTCACTCAATGGAGATCAGCCTGCAGACCAA  
 TCTGCAGAGCGTATGCAGGACAAAATTTTCATCTGAACATCATCCCTTTTTTGGATCCC  
 GTCAAACGTTGTTGCAACGCGGGGTTTTGCCGCTTCGGATGCACGCCTTGTTGTTGG

TGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGATTG  
CAGT (SEQ ID NO:82)

**Translation:**

5 MMSKLGVLIIICLFLFPLTAVQLNGDQPADQSAERMQDKISSEHHPFFDPVKRCCNAGF  
CRFGCTPCCW (SEQ ID NO:83)

**Toxin Sequence:**

10 Cys-Cys-Asn-Ala-Gly-Phe-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:84)

**Name:** Di3.1  
**Species:** distans  
**Cloned:** Yes

**DNA Sequence:**

15 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTT  
TCTGCTTCTGTTTCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCCGCAGACGG  
20 ACTTGCAGAGCGCATGCAGGACGACAGTTCAGCTGCACTGATTAGAGACTGGCTTC  
TTCAAACCCGACAGTGTGTGTGCATCCATGCCCATGCACGCCTTGCTGTAGATGAC  
25 CAGCTTTGTCATCGCGGCTACGTCAAGTATCTAATGAATAAGTAAGTAAAACGATTG  
CAGT (SEQ ID NO:85)

**Translation:**

25 MMSKLGVLITIFLLLFPILTAVPLDGDQPADGLAERMQDDSSAALIRDWLLQTRQCCVH  
PCPCTPCCR (SEQ ID NO:86)

**Toxin Sequence:**

30 Xaa2-Cys-Cys-Val-His-Xaa3-Cys-Xaa3-Cys-Thr-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:87)

**Name:** E3.1  
**Species:** ermineus  
**Cloned:** Yes

**DNA Sequence:**

35 ACCTCAAGAGGGATCGATCGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACC  
ATCTGTCTGCTTCTGTTTCCCATTAATGCTCTTCTGATGGATGGAGATCAGCCTGCAG  
40 ACCGACCTGCAGAGCGTACGGAGGATGACATTTCATCTGACTACATTCCCTGTTGCA  
GTTGGCCATGCCCCCGATACTCCAACGGTAAACTTGTTTGTGTTTGTGCTTGGATG  
ATAATGTGTTGATGACCAACTTTGTTATCACGGCTACGTCAAGTGTCTACTGAATAA  
GTAAAATGATTGCAGTA (SEQ ID NO:88)

**Translation:**

45 MMSKLGALLTICLLLPITALLMDGDQPADRPAERTEDDISSDYIPCCSWPCPRYSNGKL  
VCFCLG (SEQ ID NO:89)

**Toxin Sequence:**

Cys-Cys-Ser-Xaa4-Xaa3-Cys-Xaa3-Arg-Xaa5-Ser-Asn-Gly-Lys-Leu-Val-Cys-Phe-Cys-Cys-Leu-# (SEQ ID NO:90)

5

**Name:** Ge3.2  
**Species:** generalis  
**Cloned:** Yes

10 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC  
 TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC  
 AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTC  
 ACGTTCTGCAACTTTGGATGCCAACCTTGTTGCCTCACCTGATAACGTGTTGATGAC  
 CAACTTTCTCGAG (SEQ ID NO:91)

15 **Translation:**

GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT  
 FCNFGCQPCCLT (SEQ ID NO:92)

20 **Toxin Sequence:**

Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Leu-Thr-^ (SEQ ID NO:93)

**Name:** Ge3.3  
**Species:** generalis  
**Cloned:** Yes

25 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGGTTCTGTTTCCCC  
 TTACTGCTCTTCCACTGGATGGAGAACAACCTGTAGACCGACATGCCGAGCATATGC  
 AGGATGACAATTCAGCTGCACAGAACCCCTGGGTTATTGCCATCAGACAGTGTTC  
 ACGTTCTGCAACTTTGGATGCCAGCCTTGTTGCGTCCCCTGATAACGTGTTGATGAC  
 CAACTTTCTCGAG (SEQ ID NO:94)

30 **Translation:**

GSMMSKLGVLLTICLVLFPLTALPLDGEQPVDRHAEHMQDDNSAAQNPWVIAIRQCCT  
 FCNFGCQPCCVP (SEQ ID NO:95)

35 **Toxin Sequence:**

Xaa2-Cys-Cys-Thr-Phe-Cys-Asn-Phe-Gly-Cys-Gln-Xaa3-Cys-Cys-Val-Xaa3-^ (SEQ ID NO:96)

**Name:**  $\mu$ -GIIIA  
**Species:** geographus  
**Cloned:** Yes

**DNA Sequence:**

GTCGACTCTAGAGGATCCGACAACAAAGAGTCAACCCCACTGCCACGTCAAGAGCG  
 AAGCGCCACAGCTAAGACAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGG  
 5 AGTCTTGTTGACCATCTGTCTGCTTCTGTTTCJCCTTACTGCTCTTCCGATGGATGGA  
 GATGAACCTGCAAACCGACCTGTCGAGCGTATGCAGGACAACATTTTCATCTGAGCA  
 GTATCCCTTGTTTGAGAAGAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAG  
 ACCGACAATGCAAACCCCAAGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAA  
 CTTTATCACGGCTACGTCAAGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCT  
 10 CAGATTTGCTTTTGTGTTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGATGCG  
 GATTGTCATATATTTCTCGATTCCAATCCAACACTAGATGATTTAATCACGATAGAT  
 TAATTTTCTATCAATGCCTTGATTTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATT  
 TTTTCGTCACTGTCTACACAAACGCATGCATGCACGCATGCACGCACACACGCACGC  
 ACGCTCGCACAAACATGCGCGCGCACGCACACACACACACACACACAAACACA  
 15 CACACAAGCAATCACACAATTATTGACATTATTTATTTATTTCATTGATGTATTTGTTA  
 TTCGTTTGCTTGTTTTTAGAATAGTTTGAGGCCGCTTTTTTGGAATTTATTTGAACTGC  
 TTTATTGTATACGAGTACTTCGTGCTTTGAAACACTGCTGAAAATAAAACAAACACT  
 GACGTAGC (SEQ ID NO:97)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK  
 KCKDRQCKPQRCCAGR (SEQ ID NO:98)

**Toxin Sequence:**

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-  
 Cys-Cys-Ala-# (SEQ ID NO:99)

**Name:**  $\mu$ -GIIB  
**Species:** geographus  
**Isolated:** Yes  
**Cloned:** Yes

**DNA Sequence:**

GGCCAGACGACAACAAAGAGTCAACCCCACTGCCACGTCAAGAGCGAAGCGCCAC  
 AGCTAAGACAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTT  
 GACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCT  
 GCAAACCGACCTGTCGAGCGTATGCAGGACAACATTTTCATCTGAGCAGTATCCCTTG  
 TTTGAGAAGAGACGAGATTGTTGCACTCCGCCGAGGAAATGCAAAGACCGACGATG  
 35 CAAACCCATGAAATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACG  
 GCTAGCTCAGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCTCAGATTGCTTT  
 TGTGTTTTGGTCTAAGATCAATGACCAAACCGTTGTTTTGATGCGGATTGTCATATA  
 TTTCTCGATTCCAATCCAACACTAGATGATTTAATCACGATAGATTAATTTTCTATCA  
 40 ATGCCTTGATTTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATTTTTCGTCACTGT  
 CTACACAAACGCATGCATGCACGCATGCACGCACACACACACACACAAACACACACACGAAGCAATC  
 45 ACATGCGCGCGCACGCACACACACACACACACACACACACACACGAAGCAATC  
 ACACAATTAGTTGACATTATTTATTTATTTCATTGATGTATTTGTTATTCGTTTGCTTGT

TTTTAGAATAGTTTGAGGCCGTCTTTTGGATTATTTGAACTGCTTTATTGTATACG  
AGTACTTCGTGCTTTGAAACACTGCTGAAAATAAAACAAACACTGACGTAGCAAAA  
AAAAAAA (SEQ ID NO:100)

5 **Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPR  
KCKDRRCKPMKCCAGR (SEQ ID NO:101)

**Toxin Sequence:**

10 Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Arg-Cys-Lys-Xaa3-Met-Lys-  
Cys-Cys-Ala-# (SEQ ID NO:102)

**Name:**  $\mu$ -GIIC

**Species:** geographus

**Isolated:** Yes

**Toxin Sequence:**

20 Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Arg-Cys-Lys-Xaa3-Leu-Lys-  
Cys-Cys-Ala-# (SEQ ID NO:103)

**Name:** Gm3.1

**Species:** gloriamaris

**Cloned:** Yes

**DNA Sequence:**

30 CTCACTATAGGAATTCGAGCTCGGTACACGGGATCGATAGCAGTTCATGATGTCTAA  
ACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTG  
GATGGAGATCAACATGCAGACCAACCTGCAGAGCGTCTGCATGACCGCCTTCCAAC  
TGAAAATCATCCCTTATATGATCCCGTCAAACGGTGTGCGATGATTGGAATGCGA  
CTATTCTTGCTGGCCTTGCTGTATGTTTGGATAACCTTTGTTATCGCGGCCTCGATAA  
GTGTCTAATGAATAAGTAAAACGATTGCAGTAGGC (SEQ ID NO:104)

**Translation:**

35 MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLHDRLPTENHPLYDPVKRCCDDSE  
CDYSCWPCCMFG (SEQ ID NO:105)

**Toxin Sequence:**

40 Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Met-Phe-# (SEQ ID  
NO:106)

**Name:** Gm3.2

**Species:** gloriamaris

**Cloned:** Yes

**DNA Sequence:**

GTTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTGTCTACTTCTGTTTCCCCTT  
 ACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGATATGCAGAGCGTATGCA  
 5 GGACGACATTTTCATCTGAACATCATCCCATGTTTGATGCCGTCAGAGGGTGTTGCCA  
 TCTGTTGGCATGCCGCTTCGGATGCTCGCCTTGTTGTTGGTGATCAGCTTTGTTATCG  
 CGGCCTCATCAAGTGACTCTAATGCAAA (SEQ ID NO:107)

**Translation:**

10 MMSKLGVLLIICLLLFPLTAVPLDGDQPADRYAERMQDDISSEHHPMFDAVRGCCHLLA  
 CRFGCSPCCW (SEQ ID NO:108)

**Toxin Sequence:**

Gly-Cys-Cys-His-Leu-Leu-Ala-Cys-Arg-Phe-Gly-Cys-Ser-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID  
 15 NO:109)

**Name:** Gm3.3  
**Species:** gloriamaris  
**Cloned:** Yes

**DNA Sequence:**

GAGACGACAAGGAACAGTCAACCCACAGCCACGCCAAGAGCAGACAGCCACAGC  
 TACGTGAAGAAGGGTGGAGAGAGGTTTCGTGATGTTGAAAATGGGAGTGGTGCTATT  
 20 CATCTTCCTGGTACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGT  
 AGAACGATATGCGGAGAACAACAGCTCCTCAACCCAGATGAAAGGAGGGAAATC  
 ATATTGCATGCTCTGGGGACGCGATGCTGTTCTTGGGATGTGTGCGACCACCCGAGT  
 TGTACTTGCTGCGGCGGTTAGCGCCGAACATCCATGGCGCTGTGCTGGGCGGTTTTA  
 TCCAACAACGACAGCGTTTGTGATTTCATGTATCATTGCGCCCACGTCTCTTGTCTA  
 30 AGAATGACGAACATGATTGCACTCTGGTTCAGATTTCGTGTTCTTTTCTGACAATAA  
 ATGACAAAACCTCCAAAAAA (SEQ ID NO:110)

**Translation:**

35 MLKMGVVLFIPLVLFPLATLQLDADQPVERYAENKQLLNPDERREILHALGTRCCSWD  
 VCDHPSTCCGG (SEQ ID NO:111)

**Toxin Sequence:**

Cys-Cys-Ser-Xaa4-Asp-Val-Cys-Asp-His-Xaa3-Ser-Cys-Thr-Cys-Cys-Gly-# (SEQ ID NO:112)

40 **Name:** La3.1  
**Species:** laterculatus  
**Cloned:** Yes

**DNA Sequence:**

45 CGACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA  
 CCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGC



AGACCGACCTGCAGAGCGTATGCAGGACGTTTCATCTGAACAGCATCCCTTGTATG  
ATCCCGTCAAACGGTGTTGCGACTGGCCATGCAGCGGATGCATCCCTTGTTGCTAAT  
AGTAACAACGTGTTGATAACCAACTTTCTTACCACGACTACGTCAAGTGTCTAATGA  
ATAAGTAAAATGATTGCAGT (SEQ ID NO:113)

5

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADRP AERMQDVSSEQHPLYDPVKRCCDWPC  
SGCIPCC (SEQ ID NO:114)

10

**Toxin Sequence:**

Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ser-Gly-Cys-Ile-Xaa3-Cys-Cys-^ (SEQ ID NO:115)

**Name:** La3.2

**Species:** laterculatus

**Cloned:** Yes

**DNA Sequence:**

CGACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA  
CCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTGGATGGAGATCAACCTGCAGACC  
GACTTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGCATCCCTTTGAAAAG  
AGACGAGACTGTTGCACACCTCCGAAGAAATGCAGAGACCGACAATGCAAACCTGC  
ACGTTGTTGCGGAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCTACGTCAA  
GTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:116)

**Translation:**

MMSKLGVLLTICLLLFPLTALDGDQPADRLAERMQDDISSEQHPFEKRRDCCTPPKKCR  
DRQCKPARCCGG (SEQ ID NO:117)

30

**Toxin Sequence:**

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Arg-Asp-Arg-Gln-Cys-Lys-Xaa3-Ala-Arg-  
Cys-Cys-Gly-# (SEQ ID NO:118)

35

**Name:** La3.3

**Species:** laterculatus

**Cloned:** Yes

**DNA Sequence:**

GGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGC  
TTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACTTGACGCCGATCTGC  
AGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCACCTCTTTGAAAAGAGAC  
GACCACCATGTTGCACCTATGACGGGAGTTGCCTAAAAGAATCATGCATGCGTAAA  
GCTTGTTGCGGATGATAACGTGTTGATGACCAACTTTGTTATCACGGCTACTCAAGT  
GTCTAATGAATAAGTAAAATGATTGCAGTA (SEQ ID NO:119)

45

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDLARRSAERMQDNISSEQHHLFEKRRPPCCTYD  
GSCLKESCMRKACCG (SEQ ID NO:120)

**Toxin Sequence:**

5 Arg-Xaa3-Xaa3-Cys-Cys-Thr-Xaa5-Asp-Gly-Ser-Cys-Leu-Lys-Xaa1-Ser-Cys-Met-Arg-Lys-  
Ala-Cys-Cys-# (SEQ ID NO:121)

**Name:** La3.3A

10 **Species:** laterculatus

**Cloned:** Yes

**DNA Sequence:**

15 GGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCACCTGTCTGC  
TTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACTTGCACGCCGACCTG  
CAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAGGAGA  
CGACCACCATGTTGCACCTATGACGGGAGTTGCCTAAAAGAATCATGCAAGCGTAA  
AGCTTGTTGCGGATAATAACGTGTTGATGACCAACTTTGTTATCACGGCTACTCAAG  
20 TGTCTAATGAATAAGTAAAATGATTGCAGTA (SEQ ID NO:122)

**Translation:**

MMSKLGVLLTTCLLLFPLTALPMDGDLARRPAERMQDNISSEQHPFFERRRPPCCTYD  
GSCLKESCKRKACCG (SEQ ID NO:123)

**Toxin Sequence:**

25 Arg-Xaa3-Xaa3-Cys-Cys-Thr-Xaa5-Asp-Gly-Ser-Cys-Leu-Lys-Xaa1-Ser-Cys-Lys-Arg-Lys-  
Ala-Cys-Cys-# (SEQ ID NO:124)

30 **Name:** Lp3.1

**Species:** leopardus

**Cloned:** Yes

**DNA Sequence:**

35 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC  
TACTGCTCTTTCGGCTGGTTGGAGATCAACCTGCAGAGCGACCTGCAAAGCGTACGC  
AGGACGACATTCCAGATGGACAGCATCCGTTAAATGATAGGCAGATAAACTGTTGC  
CCGTGGCCATGCCCTAGTACATGCCGCCATCAATGCTGCCATTAATGATAACGTGTT  
40 GATGACCAACTTTCTCGAG (SEQ ID NO:125)

**Translation:**

GSMMSKLGVLLTVCLLLFPLTALRLVGDQPAERPAKRTQDDIPDGQHPLNDRQINCCP  
WPCPSTCRHQCH (SEQ ID NO:126)

**Toxin Sequence:**

45 Xaa2-Ile-Asn-Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Xaa3-Ser-Thr-Cys-Arg-His-Gln-Cys-Cys-His-^  
(SEQ ID NO:127)

**Name:** Lv3.1  
**Species:** lividus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC  
 TTAAGTCTCTTCGGCTGGTTAGAGATCAACCTGCAGAGCGACCTGCAAAGCGTACGC  
 AGGACGACATTCCAAATGGACAGGATCCGTTAATTGATAGGCAGATAAATTGTTGC  
 CCTTGGCCATGCCCTGATTCATGCCACTATCAATGCTGCCACTGATAACGTGTTGAT  
 GACCAACTTTCTCGAG (SEQ ID NO:128)

**Translation:**

GSMMSKLGVLLTVCLLLFPLTALRLVRDQPAERPAKRTQDDIPNGQDPLIDRQINCCPW  
 PCPDSCHYQCCH (SEQ ID NO:129)

**Toxin Sequence:**

Xaa2-Ile-Asn-Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Xaa5-Gln-Cys-Cys-His-^  
 (SEQ ID NO:130)

**Name:** L3.1  
**Species:** lynceus  
**Cloned:** Yes

**DNA Sequence:**

AAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTG  
 CTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAATCTGCAGACCGACTTG  
 CAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGA  
 GGACGAGACTGTTGCACACCTCCGAGGAAATGCAGAGACCGAGCCTGCAAACCTCA  
 ACGTTGTTGCGGAGGATAAGCTGTTGATGACCAACTTTGTTATACGGC (SEQ ID  
 NO:131)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQSADRLAERMQDNISSEQHPFFEKRGRDCCTPP  
 RKCRDRACKPQRCCGG (SEQ ID NO:132)

**Toxin Sequence:**

Gly-Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Arg-Asp-Arg-Ala-Cys-Lys-Xaa3-Gln-  
 Arg-Cys-Cys-Gly-# (SEQ ID NO:133)

**Name:** M3.1  
**Species:** magus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATGAACCTGCAAACCG  
ACCTGTCGAGCGTATGCAGGACAACATTTTCATCTGAGCAGTATCCCTTGTTTGAGAA  
5 GAGACGAGATTGTTGCACTCCGCCGAAGAAATGCAAAGACCGACAATGCAAACCCC  
AGAGATGTTGCGCTGGACGATAACGTGTTGATGACCAACTTTATCACGGCTACGTCA  
AGTGTTTAGTGAATAAGTAAAATGATTGCAGTCTTGCTCAGATTTGCTTTTGTGTTTT  
GGTCTAAAGATCAATGACCAAACCGTTGTTTTGATGCGGATTGTCATATATTTCTCG  
ATTCCAATCCAACACTAGATGATTAAATCACGATAGATTAATTTTCTATCAATGCCT  
10 TGATTTTTTCGTCTGTCATATCAGTTTTGTTTATATTTATTTTTTCGTCACTGTCTACAC  
AAACGCATGCATGCACGCATGCACGCACACACGCACGCACGCTCGCACAAACATGC  
GCGCGCACGCACACACACACACACACACAAACACACACACACGAAGCAATCACAC  
AATTAGTTGACATTATTTATTTATTCATTGATGTATTTGTTATTCGTTTGCTTGTTTTT  
AGAATAGTTTGAGGCCGTCTTTTTGGATTTATTTGAACTGCTTTATTGTATACGAGTA  
15 CTTGTCGCGGGGAAACACTGCTGAAAATAAAACAAACACTGACGTAGCAAAAAAA  
AAAAA (SEQ ID NO:134)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDEPANRPVERMQDNISSEQYPLFEKRRDCCTPPK  
KCKDRQCKPQRCCAGR (SEQ ID NO:135)

**Toxin Sequence:**

Arg-Asp-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Gln-Cys-Lys-Xaa3-Gln-Arg-  
Cys-Cys-Ala-# (SEQ ID NO:136)

**Name:** M3.2  
**Species:** magus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA  
ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAT  
35 GAGAAAAAGGTGTTGCGGCCCGGCGGTTTCATGCCCCGTATATTTTCAGAGACAATT  
TTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGAC  
TACGCCAAGTGTCTAATGAATAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTT  
TGTATTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGTGGATTTTCATATA  
TTTCTCGAGTCCTATCCAACACTAGATGATTAAATCACGATAGATCTGATTTTTTTAT  
40 CAAAGGCTTGGTTTTTTCGTCTGTCACATCAGTTTTGTTTATATTTAATTTTTTCGTCACT  
GATTACACACACGCATGAACGCACAGAGTACTAACACATACACACACACACACACA  
CACACACACACACACACACACACACACACACACACACACGCGCGCGCGCGGCG  
CCATCTAGTAGCGCCGCGACGACACACAC (SEQ ID NO:137)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDMRKRC CGPG  
GSCP VYFRDNFICGCC (SEQ ID NO:138)

**Toxin Sequence:**

Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asn-Phe-Ile-Cys-Gly-Cys-Cys-^ (SEQ ID NO:139)

**Name:** M3.3  
**Species:** magus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGAGGGATGGAGATCAATCTGTAGACCGA  
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCTGCATCCCTTGTCATCAGA  
AAAAGAATGTGTTGCGGCGAGAGTGCGCCATGCCCCAGCTATTTTCAGAAACAGTCA  
GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCACCTTCGTTATCACGACT  
AATGATAAGTAAAATGATTGCAGTCTCGCTCAGATTTGCTTTTGTATTTTGGTCTAA  
AGATCAATGACCAAACCGTTGTTTTGATGTGGATTTTCATATATTTCTCGAGTCCTAT  
CCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTATCAAAGCCTTGGTTTT  
TCGTCTGTCACATCAGTTTTGTTTATATTTAATTTTTTCGTCACTGATTACACACACGC  
ATGAACGCACAGACGTACTAACACATACACACACACACACACACACACACACACAC  
ACACACACACACACACACAC (SEQ ID NO:140)

**Translation:**

MMSKLGVLLTICLLLFPLTALPRDGDQSVD RPAERMQDDISSELHPLSIRKRMCCGESAP  
CPSYFRNSQICHCC (SEQ ID NO:141)

**Toxin Sequence:**

Met-Cys-Cys-Gly-Xaa1-Ser-Ala-Xaa3-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-  
Cys-Cys-^ (SEQ ID NO:142)

**Name:** M3.4  
**Species:** magus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA  
ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAA  
GAGACAAAAGTGTTGCGGCCCCGCGGTTTCATGCCCCGTATATTTACAGACAATTT  
TATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCATTATCACGACT  
ACGCCAAGTGTCTAATGAATAAATAAATGATTGCAGTCTCGCTCAGATTTGCTTTT  
GTATTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGCTGGATTTTTCATATA  
TTTCTCGATTCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTTTAT  
CAATGCCTTAATTTTTTGTCTGTCTATCATATCAGTTTTGTTTATAT (SEQ ID NO:143)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCGPG  
GSCP VYFTDNFICGCC (SEQ ID NO:144)

5 **Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Thr-Asp-Asn-Phe-Ile-Cys-  
Gly-Cys-Cys-^ (SEQ ID NO:145)

10 **Name:** M3.5  
**Species:** magus  
**Cloned:** Yes

**DNA Sequence:**

15 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCTTACTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCA  
ACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAA  
GAGACAAAAGTGTTGCGGCCCGGCGGTTTCATGCCCCGTATATTTTCAGAGACAATTT  
TATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCATCTTCATTATCACGACT  
20 ACGCCAAGTGCTAATGAATAAATAAAATGATTGCAGTCTCGCTCAGATTTGCTTTT  
GTATTTTGGTCTAAAGATCAATGACCAAACCGTTGTTTTGGTGTGGATTTTCATATAT  
TTCTCGATTCTATCCAACACTAGATGATTTAATCACGATAGATCTGATTTTTT (SEQ  
ID NO:146)

**Translation:**

25 MMSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCGPG  
GSCP VYFRDNFICGCC (SEQ ID NO:147)

**Toxin Sequence:**

30 Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Gly-Ser-Cys-Xaa3-Val-Xaa5-Phe-Arg-Asp-Asn-Phe-Ile-  
Cys-Gly-Cys-Cys-^ (SEQ ID NO:148)

**Name:** U001  
35 **Species:** magus  
**Isolated:** No

**Toxin Sequence:**

40 Xaa2-Lys-Cys-Cys-Ser-Gly-Gly-Ser-Cys-Xaa3-Leu-Xaa5-Phe-Arg-Asp-Arg-Leu-Ile-Cys-Xaa3-  
Cys-Cys-^ (SEQ ID NO:149)

**Name:** Comatose/Death  
**Species:** marmoreus  
45 **Isolated:** Yes

**Toxin Sequence:**

Ser-Lys-Gln-Cys-Cys-His-Leu-Ala-Ala-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Asn-^ (SEQ ID NO:150)

5 **Name:** Mr3.1  
**Species:** marmoreus  
**Cloned:** Yes

**DNA Sequence:**

10 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCGTTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGA  
CTTGTAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAG  
AGAAGAGGAGGCTGTTGCACACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAAC  
CTGCACGTTGCTGCGGCCAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCT  
15 ACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAG (SEQ ID NO:151)

**Translation:**

MMSKLGVLLTICLLFPVTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP  
RKCKDRACKPARCCGPG (SEQ ID NO:152)

**Toxin Sequence:**

Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-  
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:153)

25 **Name:** Mr3.2  
**Species:** marmoreus  
**Cloned:** Yes

**DNA Sequence:**

30 GAGCTCGGTACCCCGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTG  
GGAATCTTGTTGACCATCTGTCTACTTCTATTTCCCTTACTGCTGTTCCGCTGGATG  
GAGATCAACCTGCAGACCGACCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAA  
CATCATCCCTTTTTTGGATCCCGTCAAACGGTGTGTCAGGTTATCATGCGGCCTGGGA  
35 TGCCACCCTTGTTGTGGATGACCAGCTTGTGTTATCGCGGCCTCATCAAGTGTCTAAT  
GAATAAGTAAAA (SEQ ID NO:154)

**Translation:**

40 MMSKLGILLTICLLLFPLTAVPLDGDQPADRPAERMQDDISSEHHPFFDPVKRCCRLSCG  
LGCHPCCG (SEQ ID NO:155)

**Toxin Sequence:**

Cys-Cys-Arg-Leu-Ser-Cys-Gly-Leu-Gly-Cys-His-Xaa3-Cys-Cys-# (SEQ ID NO:156)

45 **Name:** Mr3.3  
**Species:** marmoreus

**Cloned:** Yes

**DNA Sequence:**

5 GGCCTACACCAAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCCCCGATCGATA  
GCAGTTCATGATGTCTAGACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCC  
CTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCCGACCGACCTGCAGAGCGCCTG  
CAGGACGACATTTTCATCTGAACATCATCCCCATTTTGATTCCGGCAGAGAGTGTTGC  
GGTTCGTTTCGCATGCCGCTTTGGATGCGTGCTTGTTGTGTATGACCAGCTTTGTTAT  
CACGGCCTCATCGAGTGTCTAATGAATAAGTAAAACGATTGCAGTAGGCGGGTACC  
10 GAGCTCGAATTCC (SEQ ID NO:157)

**Translation:**

MMSRLGVLLTICLLLFPLTAVPLDGDQPADRPAERLQDDISSEHHPHFDSGRECCGSFAC  
RFGCVPCCV (SEQ ID NO:158)

**Toxin Sequence:**

Xaa1-Cys-Cys-Gly-Ser-Phe-Ala-Cys-Arg-Phe-Gly-Cys-Val-Xaa3-Cys-Cys-Val-^ (SEQ ID  
NO:159)

**Name:** Mr3.4  
**Species:** marmoreus  
**Cloned:** Yes

**DNA Sequence:**

CGACCTCAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGA  
CCATCTGTCTACTTCTATTTCCCCCTTACTGCTGTTCCGCTGGATGGAGACCAACCTGC  
AGACCGACCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAACGTCATCCTTTTTT  
TGATCGCAGCAAACAGTGTTGCCATCTGCCGGCATGCCGCTTCGGATGTACGCCTTG  
30 TTGTTGGTGATCAGCTTTGTTATCGCGTCCTCATCAAGTGTCTAATGAATAAGTAAA  
ATGATTGCAG (SEQ ID NO:160)

**Translation:**

MMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDDISSERHPFFDRSKQCCHLPA  
35 CRFGCTPCCW (SEQ ID NO:161)

**Toxin Sequence:**

Ser-Lys-Gln-Cys-Cys-His-Leu-Xaa3-Ala-Cys-Arg-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-Xaa4-^  
(SEQ ID NO:162)

**Name:** Mr3.5  
**Species:** marmoreus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC



TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCAACGTGCAGAGCGTACG  
CAGGCCGAGAAGCATTCTTGCCTGATCCGAGAATGGGCTGTTGCCCGTTTCCATGC  
AAAACCAGTTGCACTACTTTGTGTTGCGGGTGATGATAACGTGTTGATGACCAACTT  
TCTCGAG (SEQ ID NO:163)

5

**Translation:**

GSMMSKLGVLLTICLLLFPLTALPLDGDQPADQRAERTQAEKHSLPDPRMGCCPFCKT  
SCTTLCCG (SEQ ID NO:164)

10 **Toxin Sequence:**

Met-Gly-Cys-Cys-Xaa3-Phe-Xaa3-Cys-Lys-Thr-Ser-Cys-Thr-Thr-Leu-Cys-Cys-# (SEQ ID  
NO:165)

15

**Name:** U014  
**Species:** marmoreus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Cys-His-Xaa4-Asn-Xaa4-Cys-Asp-His-Leu-Cys-Ser-Cys-Cys-Gly-Ser-^ (SEQ ID NO:166)

**Name:** U017  
**Species:** marmoreus  
**Cloned:** Yes

**DNA Sequence:**

GCCAAGCTTGCATGCCTGCAGGATGACTCTAGAGGATCCCCACCTCAAGAGGGATC  
GATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTT  
TGCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAACG  
TATGCAGGACGACATTTTCATCTGAACGTCATCCCATGTTTGATGCCGTCAGAGATTG  
TTGCCCGTTGCCGGCATGCCCCTTTGGATGCAACCCTTGTTGTGGATGACCAGCTTT  
GTTATCGGGACCTCATCAAGTGTCTAATGAATAAGTAAAAAACGATTCGAGTGGGT  
ACCGAGCTCGAATTCC (SEQ ID NO:167)

35

**Translation:**

MMSKLGVLLTICLLLFALTA VPLDGDQPADRPAERMQDDISSERHPMFDAVRDCCPLP  
ACPFGCNPCCG (SEQ ID NO:168)

40 **Toxin Sequence:**

Asp-Cys-Cys-Xaa3-Leu-Xaa3-Ala-Cys-Xaa3-Phe-Gly-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID  
NO:169)

45

**Name:** U019  
**Species:** marmoreus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:170)

5

**Name:** U020  
**Species:** marmoreus  
**Isolated:** Yes

10

**Toxin Sequence:**

Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:171)

**Name:** U022  
**Species:** marmoreus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Cys-Ala-Xaa3-Ser-Ala-Cys-Arg-Leu-Gly-Cys-Arg-Xaa3-Cys-Cys-Arg-^ (SEQ ID NO:172)

**Name:** U024  
**Species:** marmoreus  
**Isolated:** Yes

**Toxin Sequence:**

Gly-Cys-Cys-Gly-Ser-Phe-Ala-Cys-Arg-Phe-Gly-Cys-Val-Xaa3-Cys-Cys-Val-^ (SEQ ID NO:173)

30

**Name:** Nb3.1  
**Species:** nobilis  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC  
 TTACTGCTCTTCCGCTGGATGAAGATCAACCGGTACACCGACCTGCAGAGCGTATGC  
 AGGACATTTTCATCTGATCAACATCTCTTCTTTGATCTCATCAAACGGTGCTGCGAGT  
 TGCCATGCGGGCCAGGCTTTTGCCTCCCTTGTTGCTGACATCAATAACGTGTTGATG  
 ACCAACTTTCTCGAG (SEQ ID NO:174)

**Translation:**

GSMMSKLGVLLTICLLLFPLTALPLDEDQPVHRPAERMQDISSDQHLFFDLIKRCCELPC  
 GPGFCVPCC (SEQ ID NO:175)

45

**Toxin Sequence:**

Cys-Cys-Xaa1-Leu-Xaa3-Cys-Gly-Xaa3-Gly-Phe-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:176)

**Name:** Nb3.2  
**Species:** nobilis  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC  
 TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC  
 AGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA  
 CTGGGAAGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT  
 GGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:177)

**Translation:**

GSMMSKLGVLLTICLLLFPLTAFPMDDGDQPADQPADRMQDDISSEQYPLFDKRQKCCT  
 GKKGSCSGKACKNLKCCSGR (SEQ ID NO:178)

**Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-  
 Cys-Cys-Ser-# (SEQ ID NO:179)

**Name:** Pu3.1  
**Species:** pulicarius  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTTTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC  
 AGGACATTGCAACTGAACAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCAACA  
 GCTGTTACATGGGATGCATCCCTTGTTGCTTCTAGTAATAACGTGTTGATGACCAAC  
 TTTCTCGAG (SEQ ID NO:180)

**Translation:**

GSMMSKLGVLLTICLLLFPLTAVPLDGDQPADRPAERMQDIATEQHPFFDPVKRCCNSC  
 YMGCI PCCF (SEQ ID NO:181)

**Toxin Sequence:**

Cys-Cys-Asn-Ser-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:182)

**Name:** Qc3.1  
**Species:** quercinus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC

TTACAGCTCTTCAGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTACG  
CAGGACATTGCATCTGAACAGTATCGAAAGTTTGATCAGAGACAGAGGTGTTGCCA  
GTGGCCATGCCCCGGTAGTTGCAGATGCTGCCGTACTGGTTAACGTGTTGATGACCA  
ACTTTCTCGAG (SEQ ID NO:183)

5

**Translation:**

GSMMSKLGVLITICLLLFPLTALQLDGDQPADRPAERTQDIASEQYRKFDQRQRCCQW  
PCPGSCRCRTG (SEQ ID NO:184)

10

**Toxin Sequence:**

Xaa2-Arg-Cys-Cys-Gln-Xaa4-Xaa3-Cys-Xaa3-Gly-Ser-Cys-Arg-Cys-Cys-Arg-Thr-# (SEQ ID NO:185)

15

**Name:** QcIIIA  
**Species:** quercinus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Cys-Ser-Gln-Asp-Cys-Leu-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-# (SEQ ID NO:186)

**Name:** QcIIIB  
**Species:** quercinus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Cys-Ser-Arg-His-Cys-Xaa4-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Asn-? (SEQ ID NO:187)

30

**Name:** R3.1  
**Species:** radiatus  
**Isolated:** Yes  
**Cloned:** Yes

35

**DNA Sequence:**

TCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCT  
GTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGTAGACCG  
ACTTGCAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATACTTCTTTGAAAA  
GAGACTACCATCGTGTTGCTCCCTTAACTTGC GGCTTTGCCAGTACCAGCATGCAA  
ACGTAACCTTGTTGCACAGGATAACGTGTTGATGACCAACTTTGTTATCACGGCTA  
CGTCAAGTGTCTAGTGAATAAGTAAAAAATTGTCAGT (SEQ ID NO:188)

40

**Translation:**

MMSKLGVLITICLLLFPLTALPMDGDQPVDRLAERMQDNISSEQHTFFEKRLPSCCSLN  
LRLCPVPACKRNPCTG (SEQ ID NO:189)

45

**Toxin Sequence:**

Leu-Xaa3-Ser-Cys-Cys-Ser-Leu-Asn-Leu-Arg-Leu-Cys-Xaa3-Val-Xaa3-Ala-Cys-Lys-Arg-Asn-Xaa3-Cys-Cys-Thr-# (SEQ ID NO:190)

5

**Name:** R3.2  
**Species:** radiatus  
**Cloned:** Yes

10 **DNA Sequence:**

AGGTCGACTCTAGAGGATCCCCAAGGATCGATAGCAGTTCATGATGTCTAAACTGG  
 GAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGG  
 AGATCAACCTGCAGACCGACTTGCAGAGCGTATGCAGGACGACATTCATCTGAGC  
 AGCATCCCTTCTTTAAAAAGAGACAACAAAGATGTTGCACCGTTAAGAGGATTTGT  
 CCAGTACCAGCATGCAGAAGTAAACCTTGTGCAAATCATAACGTATTGATGACCA  
 ACTTTGTTATCACGGCTACGTCAAGTGTCTAGTGAATAAGTAAAATGATTGCAG  
 (SEQ ID NO:191)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADRLAERMQDDISSEQHPFFKKRQRCCTV  
 KRICPVPACRSKPCKS (SEQ ID NO:192)

**Toxin Sequence:**

Xaa2-Gln-Arg-Cys-Cys-Thr-Val-Lys-Arg-Ile-Cys-Xaa3-Val-Xaa3-Ala-Cys-Arg-Ser-Lys-Xaa3-Cys-Cys-Lys-Ser-^ (SEQ ID NO:193)

25  
**Name:** R3.3  
**Species:** radiatus  
**Cloned:** Yes

**DNA Sequence:**

ACCTCAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACC  
 ATCTGTCTGCTTCTGTTTCCCGTTACTGCTCTTCCGATGGATGGTGATCAACCTGCAG  
 ACCGACTTGTAGAGCGTATGCAGGACAACATTCATCTGAGCAGCATCCCTTCTTTG  
 AAAAGAGAAGAGGAGGCTGTTGCACACCTCCGAGGAAATGCAAAGACCGAGCCTG  
 CAAACCTGCACGTTGCTGCGGCCAGGATAACGTGTTGATGACCAACTTTGTTATCA  
 CGGCTACGTCAAGTGTCTAGTGAATAAGTAAACGATTGCAGT (SEQ ID NO:194)

40 **Translation:**

MMSKLGVLLTICLLLPVTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP  
 RKCKDRACKPARCCGPG (SEQ ID NO:195)

**Toxin Sequence:**

45 Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:196)

**Name:** Ra3.1  
**Species:** rattus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGGTGACCATCTGCCTGCTTCTGTTCCCT  
 CTTGCTGCTTTTCCACTGGATGGAGATCAACCTGCAGACCACCCTGCAAAGCGTACG  
 CAAGATGACAGTTCAGCTGCCCTGATCAATGCCTGGCTTGATGAATCCCAGACTTGC  
 TGCAGTAACTGCGGTGAAGATTGTGATGGTTGTTGCCAGTAACGTGTTGATGACCAA  
 CTTTCTCGAG (SEQ ID NO:197)

**Translation:**

GSMMSKLGVLVTICLLLFPLA AFPLDGDQPADHPAKRTQDDSSAALINAWLDESQTCCS  
 NCGEDCDGCCQ (SEQ ID NO:198)

**Toxin Sequence:**

Xaa2-Thr-Cys-Cys-Ser-Asn-Cys-Gly-Xaa1-Asp-Cys-Asp-Gly-Cys-Cys-Gln-^ (SEQ ID  
 NO:199)

**Name:** Sm3.1  
**Species:** stercusmuscarum  
**Cloned:** Yes

**DNA Sequence:**

GACCTCAAGAGGGGATCGATAGCAGTTCGTGATGTCTAAACTGGGAGTCTTGTGAC  
 CATCTGTCTGCTTCTGTTTCCTCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCA  
 GACCAACCTGCAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTTGTTT  
 GATAAGAGACAAAAGTGTTGCACTGGGAAGAAGGGGTCATGCTCCGGCAAAGCAT  
 GCAAAAATCTCAAATGTTGCTCTGGACGATAACGTGTTGATGACCAACTTTGTTATC  
 ACGGCTACGTCAAGTGTCTAATGAATAAGTAAACGATTGCAGT (SEQ ID NO:200)

**Translation:**

MSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQDDISSEQYPLFDKRQKCCTGKK  
 GSCSGKACKNLKCCSGR (SEQ ID NO:201)

**Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-  
 Cys-Cys-Ser-# (SEQ ID NO:202)

**Name:** U034  
**Species:** stercusmuscarum  
**Isolated:** Yes  
**Cloned:** Yes

**DNA Sequence:**

GATCGATAGCAGTTCGTGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTT  
 CTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCA  
 5 GATCGTATGCAGAACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAA  
 AAGTGTGCGGCCCCGGCGCGTCATGCCCCAGATATTTCAAAGACAATTTTATTTGT  
 GGTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACTTCGCCAA  
 GTGTCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:203)

**Translation:**

MSKLGVLLTICLLLFPLTALPMDGDQPADQPADRMQNDISSEQYPLFDKRQKCCGPGAS  
 CPHYFKDNFICGCC (SEQ ID NO:204)

**Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Gly-Xaa3-Gly-Ala-Ser-Cys-Xaa3-Arg-Xaa5-Phe-Lys-Asp-Asn-Phe-Ile-  
 Cys-Gly-Cys-Cys-^ (SEQ ID NO:205)

**Name:** S3.1  
**Species:** striatus  
**Cloned:** Yes

**DNA Sequence:**

CGACCTTTCAAGAGGGATCGATAGCAGTTCGCGATGTCTAAACTGGGGGTATTGTTG  
 ACCATCTGTCTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGAAGATCAACCTG  
 CAGACCAACTTGAAGATCGTATGCAGGACGACATTTTCATCTGAGCAGTATCCCTCGT  
 TTGTTAGGAGACAAAAGTGTGCGGCGAAGGCTCGTCATGCCCCAAATATTTCAA  
 AACAATTTTATTTGTGGTTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTA  
 TCACGACTACGCCAAGTGTCTTGTCTAATGATAATAAAATGATTCC (SEQ ID NO:206)

**Translation:**

MSKLGVLLTICLLLFPLTALPMDEDQPADQLEDQMDDISSEQYPSFVRRQKCCGEGSS  
 CPKYFKNNFICGCC (SEQ ID NO:207)

**Toxin Sequence:**

Xaa2-Lys-Cys-Cys-Gly-Xaa1-Gly-Ser-Ser-Cys-Xaa3-Lys-Xaa5-Phe-Lys-Asn-Asn-Phe-Ile-Cys-  
 Gly-Cys-Cys-^ (SEQ ID NO:208)

**Name:** S3.2  
**Species:** striatus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTTTCCCC  
 TTAAGTCTCTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC  
 AGGACGACATTTTCATCTGACGAGCATCCCTTGTTTGATAAGAGACAAAAGTGTGCA

ATGGGGGATGCTCCAGCAAATGGTGCAGAGATCACGCACGTTGTTGCGGTCGATGA  
TAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:209)

**Translation:**

5 GSMMSKLGVLLTVCLLLFPLTALPLDGDQPADRPAERMQDDISSDEHPLFDKRQNCCN  
GGCSSKWCRDHARCCGR (SEQ ID NO:210)

**Toxin Sequence:**

10 Xaa2-Asn-Cys-Cys-Asn-Gly-Gly-Cys-Ser-Ser-Lys-Xaa4-Cys-Arg-Asp-His-Ala-Arg-Cys-Cys-#  
(SEQ ID NO:211)

**Name:** Ts3.1

**Species:** tessulatus

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATGTGTCTGCTTCTGTTTCCCC  
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTAGG  
CAGGACATTGCAACTGACGATCATCCTTTGTTTGATCCCGTCAAACGGTGCTGCCAC  
AAATGCTATATGGGATGCATCCCTTGTTGCATTTAGTAACGTGTTGATGACCAACTT  
TCTCGAG (SEQ ID NO:212)

**Translation:**

5 GSMMSKLGVLLTMCLLLFPLTAVPLDGDQPADRPAERRQDIATDDHPLFDPVKRCCHK  
CYMGCI PCCI (SEQ ID NO:213)

**Toxin Sequence:**

30 Cys-Cys-His-Lys-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Ile-^ (SEQ ID NO:214)

**Name:** Ts3.2

**Species:** tessulatus

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTGTGCTTCTGTTTCCCC  
TTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCAACCTGCAGAGCGTACG  
CAGAACGAGCAGCATCCCTTGATGATCAGAAAAGAAAGTGTTGCCGGCCGCCATG  
40 CGCCATGAGCTGCGGCATGGCTAGGTGTTGCTATTAATGATAACGTGTTGATGACCA  
ACTTTCTCGAG (SEQ ID NO:215)

**Translation:**

45 GSMMSKLGVLLTICVLLFPLTAVPLDGDQPADQPAERTQNEQHPLYDQKRKCCRPPCA  
MSCGMARCCY (SEQ ID NO:216)

**Toxin Sequence:**



Lys-Cys-Cys-Arg-Xaa3-Xaa3-Cys-Ala-Met-Ser-Cys-Gly-Met-Ala-Arg-Cys-Cys-Xaa5-^ (SEQ ID NO:217)

5   **Name:**       Circling  
     **Species:**   textile  
     **Isolated:**   Yes  
     **Cloned:**     Yes

10   **DNA Sequence:**

GAGTCAACCCACTGTCACGCCAAGAGCGGACGCCACAGCTAAGGCAAGAAGGATC  
GATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCTGTCTACTTCTGT  
TTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAACCTGCACAGC  
GTCTGCAGGACCGCATTCCAAGTGAAGATCATCCCTTATTTGATCCCAACAAACGGT  
15   GTTGCCCCGCCGGTGGCATGCAACATGGGATGCAAGCCTTGTTGTGGATGACCAGCTT  
TGTTATCGCGGTCTCATGAAGTGTCTAATGAATAAGTAAAACGATTGCAGTTTCGTT  
CAGATTTGCTGTTGTATTTTGGTCTAAAGATTAATGACCAAACCTGTTCTTTTGATCCG  
GATTTTCACGTATTTCTCGATTCTTCAACACTAGATAAGTTAATCACGACAGAT  
CTGATTTTCCATCAATGCCTTGCTTTTTGGTCTGTCATATAAATCTTGTTTATATTTAA  
20   TTTCTCGTCACTTTCAACACGCACACACACACACACACACGCGCGCGC (SEQ ID  
NO:218)

25   **Translation:**

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAQRLQDRIPTEHDHPLFDPNKRCCPPVA  
CNMGCKPCCG (SEQ ID NO:219)

30   **Toxin Sequence:**

Cys-Cys-Xaa3-Xaa3-Val-Ala-Cys-Asn-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-Gly-^ (SEQ ID NO:220)

35   **Name:**       Scratcher I  
     **Species:**   textile  
     **Cloned:**     Yes

40   **DNA Sequence:**

GGATCCAGACGACAAAGAAGAGTCAACCCACTGCCACGTCAAGAGCAGAGCCCAC  
AGCTAAGACAAGAAGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGTT  
GACCATCTGTCTCCTTCTGTTTTCCCTTAATGCTGTTCCGTTGGATGGAGATCAACCT  
40   GCAGACCAACCTGCAGAGCGTCTGCTGGACGACATTTCAATTTGAAAATAATCCCTTT  
TATGATCCCGCCAAACGGTGTTGCAGGACTTGCTTCGGTTGCACACCTTGTTGTGGA  
TGACCAGCCTCATCAAGTGTCTAACGAATAAGTAAAGCGATTGCAGTCTCGTTCAG  
ATTTACTTTTGTATTCTGGTCTAAAGATTAATGACCAAACCTCTTCTTTTGATCCGGAT  
GTACATATATTTCTCGATTCTTCAACGCTAGATAAGCTAATCACGACAGATCTG  
45   ATTTTCTGTCAATGCCTTGCTTTTTGGTCTCTCATATCACTCTTGTTTATATTTAATTT  
CTCGTCACTATATATATATACACACACACACACGGAATCCGATTGTCCAGTA  
CCGTTCTTGGGATCGAGGTATTGCTGCGATGGCTTATTCTGTACTCTTTTCTTCTGCG

CTTGATAGTGATGTCTTCTACTCCCATCTGTGCTACCCCTGGCTTGATCTTTGATAGG  
CGTGTGCCCTTCACTGGTTATAAACCCCTCTGATCCTACTCTCTGGACGCCTCGGGG  
GCCCAACCTCCAAATAAAGCGACATCCAATGAAAAAA (SEQ ID NO:221)

5 **Translation:**

MMFKLGVLITICLLLFSLNAVPLDGDQPADQPAERLLDDISFENNPFDPAKRCCRTCF  
GCTPCCG (SEQ ID NO:222)

**Toxin Sequence:**

10 Cys-Cys-Arg-Thr-Cys-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-# (SEQ ID NO:223)

**Name:** Tx3.1

**Species:** textile

**Cloned:** Yes

**DNA Sequence:**

GGAACAGTCAACCCACAGCCACGCCAAGAGCAGACAGCCACAGCTACGTGAAGA  
AGGGTGGAGAGAGGTTTCATGATGTTGAAAATGGGAGTGGTGCTATTCATCTTTCTGG  
TACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGTAGAACGATATG  
CGGAGAACAAACAGCTCCTCAACCCAGATGAAAGGAGGGAAATCCTATTGCCTGCT  
CTGAGGAAGTTCTGCTGTGATTCTGAATTGGTGCCACATTTTCGGATTGTGAGTGCTGC  
TACGGTTAGCGCCGAACATCCATGGCACTGTGCTGGGCGGTTTCATCCCAACAACG  
ACAGCGTTTGTGATTTCATGTATCATTGCGCCACGTCTCTTGTCTAAGAATGACG  
AACATGATTGCACTCTGGTTCAGATTTTCGTGTTCTTTTCTGACAATAAATGACAAAcC  
TCC (SEQ ID NO:224)

**Translation:**

MMLKMGVVLFIPLVLFPLATLQLDADQPVERYAENKQLLNPDERREILLPALRKFCDS  
NWCHISDCECCYG (SEQ ID NO:225)

**Toxin Sequence:**

Phe-Cys-Cys-Asp-Ser-Asn-Xaa4-Cys-His-Ile-Ser-Asp-Cys-Xaa1-Cys-Cys-Xaa5-# (SEQ ID NO:226)

**Name:** U031

**Species:** textile

**Isolated:** Yes

**Cloned:** Yes

**DNA Sequence:**

CAAGGAACAGTCAACCCACAGCCACGCCAAGAGCAGACAGCCACAGCTACGTGA  
AGAAGGGTGGAGAGAGGTTTCGTGATGTTGAAAATGGGAGTGGTGCTATTCATCTTC  
CTGGTACTGTTTCCCCTGGCAACGCTCCAGCTGGATGCAGATCAACCTGTAGAACGA  
TATGCGGAGAACAAACAGCTCCTCAGCCCAGATGAAAGGAGGGAAATCATATTGCA  
TGCTCTGGGGACGCGATGCTGTTCTTGGGATGTGTGCGACCAACCGAGTTGTACTTG

CTGCGGTTAGCGCCGAACATCCATGGCGCTGTGCTGGGCGGTTTTATCCCAACAACG  
 ACAGCGTTTGTGATTTCATGTATCATTGCGCCCACGTCTCTTGTCTAAGAATGACG  
 AACATGATTGCACTCTGGTTCAGATTTTCGTGTTCTTTTCTGACAATAAATGACAAAA  
 CNCC (SEQ ID NO:227)

5

**Translation:**

MLKMGVVLFIPLVLFPLATLQLDADQPVERYAENKQLLSPDERREILHALGTRCCSWD  
 VCDHPSCTCCG (SEQ ID NO:228)

10

**Toxin Sequence:**

Cys-Cys-Ser-Xaa4-Asp-Val-Cys-Asp-His-Xaa3-Ser-Cys-Thr-Cys-Cys-# (SEQ ID NO:229)

**Name:** U032

**Species:** textile

**Isolated:** Yes

**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTA CTGCTCTTCCGCTGGATGGAGATCAACCCGCAGACCAAGCTGCAGAGCGTATG  
 CAGGCCGAGCAGCATCCCTTGTTTGATCAGAAAAGACGGTGCTGCAAGTTTCCATG  
 CCCC GATAGTTGCAGATATTTGTGTTGCGGGTGATGATAACGTGTTGATGACCAACT  
 TTCTCGAG (SEQ ID NO:230)

**Translation:**

GSMMSKLGVLLTICLLLFPLTALPLDGDQPADQAAERMQAEQHPLFDQKRRCKFPCP  
 DSCRYLCCG (SEQ ID NO:231)

30

**Toxin Sequence:**

Arg-Cys-Cys-Lys-Phe-Xaa3-Cys-Xaa3-Asp-Ser-Cys-Arg-Xaa5-Leu-Cys-Cys-# (SEQ ID NO:232)

35

**Name:** T3.1

**Species:** tulipa

**Cloned:** Yes

**DNA Sequence:**

CGACCTCAAGAGGGATCGATAGCAGTTCATGTCTAAACTGGGAGTCTTGTTGACAA  
 TCTGTCTGCTTCTGTTTCCCCTTACTGCTCTGCCGATGGATGGAGATGAACCTGCAG  
 ACCGACCTGCAGAGCGTATGCAGGACAACATTTTCATCTGAGCAGCATCCCTTGTTTG  
 AGGAGAGACACGGATGTTGCAAGGGGCCCCGAAGGATGCTCCTCCAGAGAATGCAG  
 ACCCCAACATTGTTGCGGTCGACGATAACGTGTTGAGGGCCAACCTTGTTATCACGG  
 CTACGTCAAGTGTTTAGTGAATAAGTAAAATGATTGCAG (SEQ ID NO:233)

**Translation:**

MSKLGVLLTICLLLFPLTALPMDGDEPADRPAERMQDNISSEQHPLFEERHGCKKGPEG  
CSSRECRPQHCCGRR (SEQ ID NO:234)

**Toxin Sequence:**

5 His-Gly-Cys-Cys-Lys-Gly-Xaa3-Xaa1-Gly-Cys-Ser-Ser-Arg-Xaa1-Cys-Arg-Xaa3-Gln-His-  
Cys-Cys-# (SEQ ID NO:235)

**Name:** Fi3.1

10 **Species:** figulinus

**Cloned:** Yes

**DNA Sequence:**

15 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCT  
GTCTGCTTCTGATTCCCCTTACTGCTCTTTCGCTGGATGGAGATCAACCTGCAGACC  
GACCTGCAGAGCGTATGCAGGATGGAATTTTCATCTGAACAGCATCCCATGTTTGATC  
CCGTCAGACGGTGTTGCCCGTGGCCATGCAACATAGGATGCGTACCTTGTTGTTGAT  
GACCAGTTTTGTTATCGCGGCCTCATCAAATGTCTAATGAATAAGTAAAACGATTGC  
AGT (SEQ ID NO:236)

**Translation:**

MMSKLGVLLTICLLLIPLTALS LDGDQPADRPAERMQDGISSEQHPMFDPVRRCCPWPC  
NIGCVPC (SEQ ID NO:237)

**Toxin Sequence:**

5 Cys-Cys-Xaa3-Xaa4-Xaa3-Cys-Asn-Ile-Gly-Cys-Val-Xaa3-Cys-Cys-^ (SEQ ID NO:238)

**Name:** Fi3.2

30 **Species:** figulinus

**Cloned:** Yes

**DNA Sequence:**

35 CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCCTGTTGACCATCTG  
TATGCTTCTGTTTCCCTTTACTGCTCTTCCGCTGGATGGAGAGCAACCTGCAGACCA  
ACCTGCAGAGCGCATGCAGTATGACATGTTACGTGCAATGAATCCCTGGTTTGATCC  
CGTCAAAAGGTGCTGCTCGAAGAACTGCGCAGTATGCATCCCTTGTTGCCCGTAACT  
GACCAGCTTGATTATCGCGGCCAAGGCTCTAATGAATAAGTAAAACGATTGCAGT  
(SEQ ID NO:239)

**Translation:**

40 MMFKLGVLLTICMLLPFTALPLDGEQPA QPAERMQYDMLRAMNPWFDPVKRCCSK  
NCAVCIPCCP (SEQ ID NO:240)

**Toxin Sequence:**

45 Cys-Cys-Ser-Lys-Asn-Cys-Ala-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-^ (SEQ ID NO:241)

**Name:** Fi3.3  
**Species:** figulinus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGAGAGTCTTGTTGACCTTATG  
TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGAATGAAGATCAACCTGCAGAGCGT  
ATGCAGGACGACAATTCATCTGAGCAGCACCCCTTGTATGACCACAAACGAAAGTG  
TTGCCGGTGGCCATGCCCCGCAAGATGCGGCTCTTGTTGCCTGTAATAACGTGTTGG  
CCAACCTTTGTTATCACGGCCACGTCAAATGTTTAATGAATAAGTAAAACGATTGCAG  
T (SEQ ID NO:242)

**Translation:**

MMSKLRVLLTLCLLLFPLTALPLNEDQPAERMQDDNSSEQHPLYDHKRKCCRWPCPAR  
CGSCCL (SEQ ID NO:243)

**Toxin Sequence:**

Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ala-Arg-Cys-Gly-Ser-Cys-Cys-Leu-^ (SEQ ID NO:244)

**Name:** Fi3.4  
**Species:** figulinus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTATG  
TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAAGCTGCAGACCG  
ACCTGCAGAGCGTATGCAGGGCATGTCATCTGAACAGCATCCCTTCTTTGATCCCGT  
CAAACGGTGTGCGAGTTGTCACGCTGCCTTGGATGCGTCCCTTGTTGCACATCTTA  
ATAACGTGTGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATA  
AGTAAAATGATTGCAGT (SEQ ID NO:245)

**Translation:**

MMSKLGVLLTLCLLLFPLTALPLDEDQAADRPAERMQGMSSSEQHPFFDPVKRCCELSR  
CLGCVPCCTS (SEQ ID NO:246)

**Toxin Sequence:**

Cys-Cys-Xaa1-Leu-Ser-Arg-Cys-Leu-Gly-Cys-Val-Xaa3-Cys-Cys-Thr-Ser-^ (SEQ ID NO:247)

**Name:** Fi3.5  
**Species:** figulinus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCTTATG  
 TCTGCTTCTGTTTCCCCTGACTGCTCTTCCGCTGGATGAAGATCAACCTGCAGACCG  
 ACCTGCAGAGCGTATGCAGGGCATGTCATCTGAACAGCATCCCTTCTTTGATCCCGT  
 CAAACGGTGTGCGAGTTGTCAAAATGCCATGGATGCGTCCCTTGTTGCATACCTTA  
 5 ATAACGTGCGGATGACCAACTGTGTTATCACGGCCACGTCAAGTGTCTAATGAATA  
 AGTAAAATGATTGCAGT (SEQ ID NO:248)

**Translation:**

MMSKLGVLLTLCLLLFPLTALPLDEDQPADRPAERMQGMSSSEQHPFFDPVKRCCELSK  
 10 CHGCVPCIP (SEQ ID NO:249)

**Toxin Sequence:**

Cys-Cys-Xaa1-Leu-Ser-Lys-Cys-His-Gly-Cys-Val-Xaa3-Cys-Cys-Ile-Xaa3-^ (SEQ ID NO:250)

15  
**Name:** Qc3.2  
**Species:** quercinus  
**Cloned:** Yes

**DNA Sequence:**

20 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTCGGAGTCTTGTTGACCATCTG  
 TCTGGTTCTGTTTCCCCTTACAGCTCTTCAGCTGGATGGAGATCAACCTGCAGACCG  
 ACCTGCAGAGCGTACGCAGGACATTTTCATCTGAACAGTATCGAAAGTTTGATCAGA  
 GACAGAGGTGTTGCCGGTGGCCATGCCCCGGTAGTTGCAGATGCTGCCGTTATCGTT  
 25 AACGTGTTGGTGACCAGCTTTGTTATCACGACCACGCCAAGTGTCTAACGAATAAGT  
 AAAATGATTGCAGT (SEQ ID NO:251)

**Translation:**

30 MMSKLGVLLTICLVLFPLTALQLDGDQPADRPAERTQDISSEQYRKFDQRQRCCRWPCP  
 GSCRCCRYR (SEQ ID NO:252)

**Toxin Sequence:**

35 Xaa2-Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Gly-Ser-Cys-Arg-Cys-Cys-Arg-Xaa5-Arg-^  
 (SEQ ID NO:253)

40  
**Name:** Qc3.3  
**Species:** quercinus  
**Cloned:** Yes

**DNA Sequence:**

45 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
 TCTGCTTCTGTTTCCCCTTACTGCTCTTCCACTGGATGGAGATCAACCTGCAGATCAA  
 TCTGCAGAGCGACCTGCAGAGCGTACGCAGGACGACATTCAGCAGCATCCGTTATA  
 TGATCCGAAAAGAAGGTGTTGCCGTTATCCATGCCCCGACAGCTGCCACGGATCTTG  
 CTGCTATAAGTGATAACATGTTGATGGCCAGCTTTGTTATCACGGCCACGTCAAGTG  
 TCTAATGAATAAGTAAAACGATTGCAGT (SEQ ID NO:254)

**Translation:**

MMSKLGVLLTICLLLFPLTALPLDGDQPADQSAERPAERTQDDIQQHPLYDPKRRCCRY  
PCPDSCHGSCCYK (SEQ ID NO:255)

**Toxin Sequence:**

Arg-Cys-Cys-Arg-Xaa5-Xaa3-Cys-Xaa3-Asp-Ser-Cys-His-Gly-Ser-Cys-Cys-Xaa5-Lys-^ (SEQ  
ID NO:256)

**Name:** Wi3.1  
**Species:** wittigi  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCA  
TACTGCTCTTCCGGTGGGTGGAGATCAGCCTGCAGACCGACTTGCAGAGCGTATGC  
AGGACGACACTTCATCTGAGCAGCATCCCTTTGAAAAGAGACTACCATCATGTTGC  
GACTTTGAGAGGCTTTGCGTAGTACCAGCATGCATACGTCATCAGTGTTGCACAGGA  
TAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:257)

**Translation:**

MMSKLGVLLTICLLLPITALPVGGDQPADRLAERMQDDTSSEQHPFEKRLPSCCDFERL  
CVVPACIRHQCTG (SEQ ID NO:258)

**Toxin Sequence:**

Leu-Xaa3-Ser-Cys-Cys-Asp-Phe-Xaa1-Arg-Leu-Cys-Val-Val-Xaa3-Ala-Cys-Ile-Arg-His-Gln-  
Cys-Cys-Thr-# (SEQ ID NO:259)

**Name:** bt3a  
**Species:** betulinus  
**Isolated:** Yes

**Toxin Sequence:**

Cys-Cys-Lys-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:260)

**Name:** T3.2  
**Species:** tulipa  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACAATCTGTCTGCTTCTGTTTCCCC  
TACTGCTCTGCCGATGGATGGAGATGAACCTGCAGACCGACCTGCAGAGCGTATG  
CAGGACAACATTTTCATCTGAGCAGCATCCCTTGTTTGAGGAGAGACACGGATGTTG

CGAGGGGCGCGAAGGGATGCTCCTCCAGAGAATGCAGACCCCAACATTGTTGCGGTC  
GACGATAACGTGTTGATGACCAACTNTCTCGAG (SEQ ID NO:261)

**Translation:**

5 MMSKLGVLLTICLLLFPLTALPMDGDEPADRPAERMQDNISSEQHPLFEERHGCCEGPK  
GCSSRECRPQHCCGRR (SEQ ID NO:262)

**Toxin Sequence:**

10 His-Gly-Cys-Cys-Xaa1-Gly-Xaa3-Lys-Gly-Cys-Ser-Ser-Arg-Xaa1-Cys-Arg-Xaa3-Gln-His-  
Cys-Cys-# (SEQ ID NO:263)

**Name:** A3.5  
**Species:** aurisiacus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTACTTCTGTTTCCCC  
TTACTGCTTTTCCGATGGATGGAGATCAACCTGCAGACCAACCTGCAGATCGTATGC  
20 AGGACGACATTTTCATCTGAGCAGTATCCCTTGTTTGATAAGAGACAAAAGTGTTGCA  
CTGGGAGGAAGGGGTCATGCTCCGGCAAAGCATGCAAAAATCTCAAATGTTGCTCT  
GGACGATAACGTGTTGATGACCAACTTTCTCGAN (SEQ ID NO:264)

**Translation:**

25 MMSKLGVLLTICLLLFPLTAFPMGDGQPADQPADRMQDDISSEQYPLFDKRQKCCTGR  
KGSCSGKACKNLKCCSGR (SEQ ID NO:265)

**Toxin Sequence:**

30 Xaa2-Lys-Cys-Cys-Thr-Gly-Arg-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Asn-Leu-Lys-  
Cys-Cys-Ser-# (SEQ ID NO:266)

**Name:** Bt3.5  
**Species:** betulinus  
35 **Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
TTACTGCTGTTCCGTTGGATGGAGATCAACCTGCAGACCAACCTGCAGAGCGTATGC  
40 AGAACGAGCAGCATCCCTCGTTTGATCAGAAAAGAAGGTGCTGCCGGTGGCCATGC  
CCCAGTATATGCGGCATGGCTAGGTGTTGCTTCGTCATGATAACGTGTTGATGACCA  
ACTTTCTCGAG (SEQ ID NO:267)

**Translation:**

45 MMSKLGVLLTICLLLFPLTAVPLDGDQPADQPAERMQNEQHPSFDQKRRCRWPCPSIC  
GMARCCFVMITC (SEQ ID NO:268)



**Toxin Sequence:**

Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Ile-Cys-Gly-Met-Ala-Arg-Cys-Cys-Phe-Val-Met-Ile-Thr-Cys-^ (SEQ ID NO:269)

**Name:** Bt3.6  
**Species:** betulinus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTGTCTGCTTCTGTTTCCCC  
 TTACTGCTGTTCCGCTGGATGGAGATCAGCCTGCAGAGCGTACGCAGATCGAGCAG  
 CATCCCTTGTTTGACCAGAAAAGAAGGTGTTGCCGGTGGCCATGCCCCAGTAGATG  
 CGGCATGGCTAGGTGTTGCTTCGTCATGATAACGTGTTGATGANCGACCTCTCNAG  
 (SEQ ID NO:270)

**Translation:**

MMSKLGVLLIICLLLFPLTAVPLDGDQPAERTQIEQHPLFDQKRRCCRWPCPSRCGMAR  
 CCFVMITC (SEQ ID NO:271)

**Toxin Sequence:**

Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Arg-Cys-Gly-Met-Ala-Arg-Cys-Cys-Phe-Val-Met-Ile-Thr-Cys-^ (SEQ ID NO:272)

**Name:** Pr3.1  
**Species:** parius  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAAGAGCGTATGC  
 AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGAGGCTGT  
 TGCACACCTCCGAAGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGCTGCGG  
 CCCAGGATAACGTGTTGATGACCAACTTCTCGCC (SEQ ID NO:273)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGGCCTPP  
 KKCKDRACKPARCCGPG (SEQ ID NO:274)

**Toxin Sequence:**

Arg-Gly-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Lys-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-Cys-Cys-Gly-Xaa3-# (SEQ ID NO:275)

**Name:** Pr3.2  
**Species:** parius  
**Cloned:** Yes

5 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
TTACTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATGC  
AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGCTGTTGC  
ACACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGTTGCGGCC  
10 AGGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:276)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQPADRLVERMQDNISSEQHPFFEKRRGCCTPPR  
KCKDRACKPARCCGPG (SEQ ID NO:277)

15 **Toxin Sequence:**

Arg-Gly-Cys-Cys-Thr-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-  
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:278)

20 **Name:** Ct3.1  
**Species:** coronatus  
**Cloned:** Yes

25 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAA  
TTACTGCCCTTCCGCTGGATGAAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC  
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGCTGCGATT  
GGCCATGCATCCCAGGATGCACCCCTTGTTGCTTGCTTGATAACGTGTTGATGACC  
30 AACTTTCTCGAG (SEQ ID NO:279)

**Translation:**

MMSKLGVLLTICLLLPITALPLDEDQPADRPAERMQDIATEQHPLFDPVKRCCDWPCIP  
GCTPCCLP (SEQ ID NO:280)

35 **Toxin Sequence:**

Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ile-Xaa3-Gly-Cys-Thr-Xaa3-Cys-Cys-Leu-Xaa3-^ (SEQ ID  
NO:281)

40 **Name:** Ms3.1  
**Species:** musicus  
**Cloned:** Yes

45 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCCTGTTGACCATCTGTCTGCTTCTGTTTCCTC  
TTTCTGCTCTTCCGATGGATGAAGATCAACTTGCAGACCTACCTGCAGAGCGTATGC

GGGACACTGCAACTGTAGATCATCCCTCCTATGATCCTGACAAAGCGTGCTGCGAG  
CAGAGCTGTACAACATGCTTTCCGTGCTGCTAGCCTTGAACACAGTAACGTGTTGAT  
GACCAACTTTCTCGAG (SEQ ID NO:282)

5 **Translation:**

MMSKLGVLLTICLLLFPLSALPMDEDQLADLPAERMRTDATTVDHPSYDPDKACCEQSC  
TTCFPCC (SEQ ID NO:283)

**Toxin Sequence:**

10 Ala-Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Phe-Xaa3-Cys-Cys-^ (SEQ ID NO:284)

**Name:** bt3b

**Species:** betulinus

**Isolated:** Yes

**Toxin Sequence:**

15 Ala-Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-^ (SEQ ID NO:285)

**Name:** bt3c

**Species:** betulinus

**Isolated:** Yes

**Toxin Sequence:**

20 Cys-Cys-Xaa1-Gln-Ser-Cys-Thr-Thr-Cys-Met-Xaa3-Cys-Cys-Xaa4-? (SEQ ID NO:286)

30 **Name:** Pn3.2

**Species:** pennaceus

**Cloned:** Yes

**DNA Sequence:**

35 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
TTACTGCTCTTCCGCTGGATGGAGATCAACCTGCATACCAAGCTGCAGAGCGTATGC  
AGGCCGAGCATCATCCCTTGTTTGATCAGAAAAGACGGTGCTGCAAGTTTCCATGCC  
CCGATAGTTGCAAATATTTGTGTTGCGGGTGATGATAACATGTTGATGACCAACTTT  
CTTGAG (SEQ ID NO:287)

**Translation:**

40 MMSKLGVLLTICLLLFPLTALPLDGDQPAYQAAERMQAEHHPLFDQKRRCKFPCPDS  
CKYLCCG (SEQ ID NO:288)

**Toxin Sequence:**

45 Arg-Cys-Cys-Lys-Phe-Xaa3-Cys-Xaa3-Asp-Ser-Cys-Lys-Xaa5-Leu-Cys-Cys-# (SEQ ID  
NO:289)

**Name:** Pu3.2  
**Species:** pulicarius  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTAGTGCTCTTCCGATGGATGGTGATCAACTTGCAGACCGACTTGTAGAGCGTATGC  
 AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGATCCCGTCAAACGGTGTTGCG  
 TCAGCTGTTACATGGGATGCATCCCTTGTTGCTTCTAGTAATAACGTGTTGATGACC  
 AACTTTCTCGAG (SEQ ID NO:290)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDLADRLVERMQDNISSEQHPFDPVKRCCVSCY  
 MGCIPCCF (SEQ ID NO:291)

**Toxin Sequence:**

Cys-Cys-Val-Ser-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:292)

**Name:** Pu3.3  
**Species:** pulicarius  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCGTCTGTCTGCTTCTGTGTCCCC  
 TTAGTGCTCTTCCACTGGATGAAGATCAACTTGCAGACCGACCTGCAGAGCGTATGC  
 AGGATGACACTTCAGCTGCACAGATTTTCGGGTTTGATCCCGTCAAACGGTGCTGCA  
 AATTGCTATGCTACTCGGGATGCACTCCTTGTTGCCATATTTGATAACGTGTTGATG  
 ACCAACTTTCTCGAG (SEQ ID NO:293)

**Translation:**

MMSKLGVLLTVCLLLCPLTALPLDEDQLADRPAERMQDDTSAAQIFGFDPVKRCKLL  
 CYSGCTPCCHI (SEQ ID NO:294)

**Toxin Sequence:**

Cys-Cys-Lys-Leu-Leu-Cys-Xaa5-Ser-Gly-Cys-Thr-Xaa3-Cys-Cys-His-Ile-^ (SEQ ID NO:295)

**Name:** Ra3.2  
**Species:** rattus  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTGTGTTTCCGC  
 TTAGTGCTCTTCCGATGGATGGTGATCAACCTGCAGACCGACTTGTAGAGCGTATAC

AGGACAACATTTTCATCTGAGCAGCATCCCTTCTTTGAAAAGAGAAGAGGCTGTTGC  
GCACCTCCGAGGAAATGCAAAGACCGAGCCTGCAAACCTGCACGTTGCTGCGGCC  
AGGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:296)

5 **Translation:**

MMSKLGVLITICLLVFPLTALPMDGDQPADRLVERIQDNISSEQHPFFEKRRGCCAPPRK  
CKDRACKPARCCGPG (SEQ ID NO:297)

**Toxin Sequence:**

10 Arg-Gly-Cys-Cys-Ala-Xaa3-Xaa3-Arg-Lys-Cys-Lys-Asp-Arg-Ala-Cys-Lys-Xaa3-Ala-Arg-  
Cys-Cys-Gly-Xaa3-# (SEQ ID NO:298)

**Name:** Sm3.3  
**Species:** stercusmuscarum  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACAATCTGTCTGCTTCTGTTTCCCC  
TTATTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC  
AGGACGACATTTTCATCTGAGAAGCATCCCTTGTTTGATAAGAGACAACGGTGTTGC  
AATGGGCGGAGGGGATGCTCCAGCAGATGGTGCAGAGATCACTCACGTTGTTGCGG  
TCGACGATAACGTGTTGATGACCAACTTTCTCGAG (SEQ ID NO:299)

**Translation:**

MMSKLGVLITICLLLFPLIALPLDGDQPADRPAERMQDDISSEKHPLFDKRQRCCNGRR  
GCSSRWCRDHSRCCGRR (SEQ ID NO:300)

**Toxin Sequence:**

30 Xaa2-Arg-Cys-Cys-Asn-Gly-Arg-Arg-Gly-Cys-Ser-Ser-Arg-Xaa4-Cys-Arg-Asp-His-Ser-Arg-  
Cys-Cys-# (SEQ ID NO:301)

**Name:** Eb3.1  
**Species:** ebraeus  
**Cloned:** Yes

**DNA Sequence:**

40 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
TTACTGCTCTTCCACTGGATGAAGGTCAACCTGCAGACCTACCTGCAGAGCGTATGC  
AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCTGTCAAACGGTGTTGCGAGC  
AGCCATGCTACATGGGATGCATCCCTTGTTGC. TCTAATAATAACGTGTTGATGACC  
AACTTTCTCGAG (SEQ ID NO:302)

45 **Translation:**

MMSKLGVLITICLLLFPLTALPLDEGQPADLPAERMQDIATEQHPLFDPVKRCCEQPCY  
MGCIPCCF (SEQ ID NO:303)

**Toxin Sequence:**

Cys-Cys-Xaa1-Gln-Xaa3-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:304)

5

**Name:** Eb3.2  
**Species:** ebraeus  
**Cloned:** Yes

10 **DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTACTGCTCTTCCACTGGATGAAGATCAACCTGCAGACCTACCTGCAGAGCGTATGC  
 AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCTGTCAAACGGTGCTGCGCGC  
 AGCCATGCTACATGGGATGCATCCCTTGTTGCTTCTAATAATAACGTGTTGATGACC  
 AACTTTCTCGAG (SEQ ID NO:305)

**Translation:**

MMSKLGVLLTICLLLFPLTALPLDEDQPADLPAERMQDIATEQHPLFDPVKRCCAQPCY  
 MGCIPCCF (SEQ ID NO:306)

**Toxin Sequence:**

Cys-Cys-Ala-Gln-Xaa3-Cys-Xaa5-Met-Gly-Cys-Ile-Xaa3-Cys-Cys-Phe-^ (SEQ ID NO:307)

**Name:** Fd3.2  
**Species:** flavidus  
**Cloned:** Yes

**DNA Sequence:**

30 GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCCC  
 TTACTGCTGTTCCGTTGGATGGAGATCAACCTGCAGACCAGCCTGCAGAGCGTATGC  
 AGAACGAGCAGCATCCCTTGTTTGATCAGAAAAGAAGGTGCTGCCGGTGGCCATGC  
 CCCAGTATATGCGGCATGGCTAGGTGTTGCTCGTCATGATAACGTGTTGATGACCAA  
 CTTTCTCGAG (SEQ ID NO:308)

35

**Translation:**

MMSKLGVLLTICLLLFPLTAVPLDGDQPADQPAERMQNEQHPLFDQKRRCCRWPCPSIC  
 GMARCCSS (SEQ ID NO:309)

40 **Toxin Sequence:**

Arg-Cys-Cys-Arg-Xaa4-Xaa3-Cys-Xaa3-Ser-Ile-Cys-Gly-Met-Ala-Arg-Cys-Cys-Ser-Ser-^  
 (SEQ ID NO:310)

45 **Name:** Mf3.1  
**Species:** miliaris  
**Cloned:** Yes

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTGTCTGCTTCTGTTTCCAA  
 TTACTGCCCTTCCACTGGATGAAGATCAACCTGCAGACCGACCTGCAGAGCGTATGC  
 5 AGGACATTGCAACTGAACAGCATCCCTTGTTTGATCCCGTCAAACGGTGTTGCGATT  
 GGCCATGCAGCGCAGGATGCTACCCTTGTTGCTTCCCTTAATAACGTGTTGATGACC  
 AACTNANGNAAAAAAAA (SEQ ID NO:311)

**Translation:**

10 MMSKLGVLLTICLLFPITALPLDEDQPADRPAERMQDIATEQHPLFDPVKRCCDWPCS  
 AGCYPCCFP (SEQ ID NO:312)

**Toxin Sequence:**

15 Cys-Cys-Asp-Xaa4-Xaa3-Cys-Ser-Ala-Gly-Cys-Xaa5-Xaa3-Cys-Cys-Phe-Xaa3-^ (SEQ ID  
 NO:313)

**Name:** Mf3.2  
**Species:** miliaris  
**Cloned:** Yes  
**Notes:**

**DNA Sequence:**

GGATCCATGATGTCTAAACTGGGAGTGGTGCCATTTCGTCTTTCTGGTCCTGTTTCCCC  
 25 TGGCAACACTCCAACCTGGATGCAGATCAACCTGCAGACCGACCTGCGCGTAAAAAG  
 GGCATTGCAACTAAACGGCATCCCTTGCTCTGATCCTGTCAGAGGGTGTTGCCCTCCA  
 ATGTGCACACCATGCTTCCCTTGCTGTTTTCGTTAATAACGTGTTGATGNATGATGN  
 AN (SEQ ID NO:314)

**Translation:**

30 MMSKLGVPFVFLVLFPLATLQLDADQPADRPARKKGIATKRHPLSDPVRGCCPPMCTPCFPCC  
 FR (SEQ ID NO:315)

**Toxin Sequence:**

35 Gly-Cys-Cys-Xaa3-Xaa3-Met-Cys-Thr-Xaa3-Cys-Phe-Xaa3-Cys-Cys-Phe-Arg-^ (SEQ ID  
 NO:316)

**Name:** Af3.1  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

45 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
 TCTGCTTCTGTTTCCCCTTACTGCTCTTCCGCTGGATGGAGATCAACCTGCAGACCA  
 AGCTGCAGAGCGTATGCAGGCCGAGCAGCATCCCTTGTTTGATCAGAAAAGACGGT  
 GTTGCAGGTTTCCATGCCCCGATACTTGCAGACATTTGTGTTGCGGGTGATGATAAC

GTGCTGATGACCCACTTTGTCATCACGGCTACGTCAAGTGTCTAATGAATAAGTAAA  
ATGATTGCAGT (SEQ ID NO:317)

**Translation:**

5 MMSKLGVLLTICLLLFPLTALPLDGDQPADQAAERMQAEQHPLFDQKRRCCRFPCPDT  
CRHLCCG (SEQ ID NO:318)

**Toxin Sequence:**

10 Arg-Cys-Cys-Arg-Phe-Xaa3-Cys-Xaa3-Asp-Thr-Cys-Arg-His-Leu-Cys-Cys-# (SEQ ID  
NO:319)

**Name:** Af3.2

**Species:** ammimalis

**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTTTAAACTGGGAGTCTTGCTGACCATCTG  
TCTACTTCTGTTTTCCCTTAATGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCA  
ACCTGCAGAGCGTCTGCTGGACGACATTCATCTGAAAATAATCCCTTTTATGATCC  
CGCCAAACGGTGTTCATGACTTGCTTCGGTTGCACACCTTGTTGTGGATGACCAGC  
CTCATCAAGTGTCTAACGAATAAGTAAAACGATTGCAGT (SEQ ID NO:320)

**Translation:**

MMFKLGVLLTICLLLFSLNAVPLDGDQPADQPAERLLDDISSENNPFYDPAKRCCMTCF  
GCTPCCG (SEQ ID NO:321)

**Toxin Sequence:**

30 Cys-Cys-Met-Thr-Cys-Phe-Gly-Cys-Thr-Xaa3-Cys-Cys-# (SEQ ID NO:322)

**Name:** Af3.3

**Species:** ammimalis

**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
AACCTGCAGAGCGTCTGCAGGACCGCCTTCCAATGAAAATCATCCCTTATATGATC  
40 CCGTCAAACGGTGTTCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTA  
TTTTTTCATAACCTTTGTTATCGCGGCCTCATCCTAGTGTCAAATGAATAAGTAAAA  
CGATTGCAGT (SEQ ID NO:323)

**Translation:**

45 MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCDDSE  
CDYSCWPCCIFS (SEQ ID NO:324)



**Toxin Sequence:**

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Phe-Ser-^ (SEQ ID NO:325)

**Name:** Af3.4  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGGATCGATAGCAGTTCATGATGTTTAAACTCGGAGTCTTGCTGACCATCTG  
 TCTACTTCTGTTTTCCCTAATGCTGTTCCGCTGGATGGAGATCAACATGCAGACCAA  
 CCTGCAGAGCGTCTGCAGGACCGCCTTCCAACCTGAAAATCATCCCTTATATGATCCC  
 GTCAAACGGTGTTGCAGGTTGTTATGCCTCAGTTGCAACCCTTGTTGTGGATGACCA  
 GCTTTGTTATCACGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATTGCAGT  
 (SEQ ID NO:326)

**Translation:**

MMFKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQDRLPTENHPLYDPVKRCCRLLC  
 LSCNPCCG (SEQ ID NO:327)

**Toxin Sequence:**

Cys-Cys-Arg-Leu-Leu-Cys-Leu-Ser-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:328)

**Name:** Af3.6  
**Species:** ammiralis  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
 GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
 AACCTGCAGAGCGTCTGCAGGACCGCATTCCAACCTGAAGATCATCCCTTATTTGATC  
 CCAACAAACGGTGTTGCGATGATTCGGAATGCGGCTATTCATGCTGGCCTTGCTGTT  
 ATGGATAAGCTTTGTTATCGCGGCCTCATCCAGTGTCAACGAATAAGTAAAACGATT  
 GCAGT (SEQ ID NO:329)

**Translation:**

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRIPTEDHPLFDPNKRCCDDSE  
 CGYSCWPCCYG (SEQ ID NO:330)

**Toxin Sequence:**

Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Gly-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa5-# (SEQ ID NO:331)

**Name:** Sf3.1  
**Species:** spurius  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCT  
 GTCTGCTTCTGTTTCCACGTACTTCTCTCCGCTGGATGGAGATCAACCTGCAGTCCG  
 ATCTGCAAAGCGTATGCATTCATCTATACAGCGTCGTTTCTTTGATCCCGTCAAACG  
 GTGTTGCCCTAGATGCAGCGAGTGCAACCCTTGTTGTGGATGACCAGCTTTGTCATC  
 GCGGCCTCATTAAGTGTCTAATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:332)

**Translation:**

MMSKLGVLLTICLLLFPRSLPLDGDQPAVRS AKRMHSSIQRFFDPVKRCCPRCSECNP  
 CCG (SEQ ID NO:333)

**Toxin Sequence:**

Cys-Cys-Xaa3-Arg-Cys-Ser-Xaa1-Cys-Asn-Xaa3-Cys-Cys-# (SEQ ID NO:334)

**Name:** Om3.1  
**Species:** omaria  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTCGTTGACCATCT  
 GTCTACTTCTATTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCA  
 ACCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCC  
 CGTCAAACGGTGTGCGATGAGGAAGAATGCAGCAGTGCATGCTGGCCTTGTTGTT  
 GGGGGTGATCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAT  
 GATTGCAGT (SEQ ID NO:335)

**Translation:**

MMSKLGVSLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCDEEE  
 CSSACWPCCWG (SEQ ID NO:336)

**Toxin Sequence:**

Cys-Cys-Asp-Xaa1-Xaa1-Xaa1-Cys-Ser-Ser-Ala-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:337)

**Name:** Om3.2  
**Species:** omaria  
**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTG  
 TCTACTTCTGTGTCCCCTTACTGCTGTTCTGGAGGATGGAGATCAACCTGCAGACCG

ACCTGCAGAGCGTATGCAGGACGACATTTCAACTGAGCATCATCCCTTTTATGATCC  
CGTCAAACGGTGTGTGCAAGTACGGGTGGACATGCTTGCTAGGATGCACTCCTTGTGA  
TTGTTGACCAGTTTTGTTATCGCGGCCTCGTCAAGTGTCTAATGAATAAGTAAAACG  
ATTGCAGT (SEQ ID NO:338)

5

**Translation:**

MMSKLGVLLIICLLLCPLTAVLEDGDQPADRPAERMQDDISTEHPFYDPVKRCCKYG  
WTCLLGCTPCDC (SEQ ID NO:339)

10

**Toxin Sequence:**

Cys-Cys-Lys-Xaa5-Gly-Xaa4-Thr-Cys-Leu-Leu-Gly-Cys-Thr-Xaa3-Cys-Asp-Cys-^ (SEQ ID NO:340)

15

**Name:** Om3.3

**Species:** omaria

**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTATACTGGGAGTCTTGTTGATCATCTG  
TCTACTTCTGTGTCCCCTTACTGCTGTTCTGGAGGATGGAGATCAACCTGCAGACCG  
ACCTGCAGAGCGTATGCAGGACGGCATTTCATCTGAACATCATCCCTTTTTGGATCC  
CGTCAAACGGTGTGTGCCATCTATTGGCATGCCGCTTTGGATGCTCGCCTTGTTGTTG  
GTGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATT  
GCAGT (SEQ ID NO:341)

**Translation:**

MMSILGVLLIICLLLCPLTAVLEDGDQPADRPAERMQDGISSEHHPFLDPVKRCCHLLAC  
RFGCSPCCW (SEQ ID NO:342)

30

**Toxin Sequence:**

Cys-Cys-His-Leu-Leu-Ala-Cys-Arg-Phe-Gly-Cys-Ser-Xaa3-Cys-Cys-Xaa4-^ (SEQ ID NO:343)

35

**Name:** Om3.4

**Species:** omaria

**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGATCATCTG  
TCTACTTCTTTGTCCCCTTACTGCTGTTCCGCAGGATGGAGATCAACCTGCAGACCG  
ACCTGCAGAGCGTATGCAGGGCGGCATTTCATCTGAACATCATCCCTTTTTTGGATCC  
CGTCAAACGGTGTGTGCAGGTACGGGTGGACATGCTGGCTAGGATGCACTCCCTGTG  
GTTGTTGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAAC  
GATTGCAGT (SEQ ID NO:344)

45

**Translation:**

MMSKLGVLLIICLLLCPLTAVPQDGDQPADRPAERMQGGISSEHHPFFDPVKRCCRYGW  
TCWLGCTPCGC (SEQ ID NO:345)

**Toxin Sequence:**

5 Cys-Cys-Arg-Xaa5-Gly-Xaa4-Thr-Cys-Xaa4-Leu-Gly-Cys-Thr-Xaa3-Cys-Gly-Cys-^ (SEQ ID NO:346)

**Name:** Ep3.1

10 **Species:** episcopatus

**Cloned:** Yes

**DNA Sequence:**

15 CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTACTTCTGTTTTCCCTTATTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA  
CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTATGCCT  
GTCAAACGGTGTGCGATGAGGACGAATGCAACAGTTCATGCTGGCCTTGTTGTTGG  
GGGTGATCAGCTTTGTTATCGCGGCCTGATCAAGTGTATAATGAATAAGTAAAACG  
20 ATTGCAGT (SEQ ID NO:347)

**Translation:**

MMSKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQGDILSEKHPLFMPVKRCCDEDE  
CNSSCWPCCWG (SEQ ID NO:348)

**Toxin Sequence:**

25 Cys-Cys-Asp-Xaa1-Asp-Xaa1-Cys-Asn-Ser-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:349)

30 **Name:** Ep3.2

**Species:** episcopatus

**Cloned:** Yes

**DNA Sequence:**

35 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTACTTCTGTTTTCCCTTATTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA  
CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTATGCCT  
GTCAAACGGTGTGCGATGAGGACGAATGCAGCAGTTCATGCTGGCCTTGTTGTTGG  
GGATGAGCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAACG  
40 ATTGCAGT (SEQ ID NO:350)

**Translation:**

MMSKLGVLLTICLLLFSLIAVPLDGDQHADQPAERLQGDILSEKHPLFMPVKRCCDEDE  
CSSSCWPCCWG (SEQ ID NO:351)

**Toxin Sequence:**

Cys-Cys-Asp-Xaa1-Asp-Xaa1-Cys-Ser-Ser-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa4-# (SEQ ID NO:352)

5 **Name:** Ep3.3  
**Species:** episcopatus  
**Cloned:** Yes

**DNA Sequence:**

10 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA  
CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCCC  
GTCAAACGGTGTGCCCCGGCGGCGGCATGTGCCATGGGATGCAAGCCTTGTTGTGG  
ATGAGCAGCTTTGTTATCGTGGCCTCATCAAGTGTCTAATGAATAAGTAAAACGATT  
15 GCAGT (SEQ ID NO:353)

**Translation:**

MMSKLGVLLTICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCPAAA  
CAMGCKPCCG (SEQ ID NO:354)

**Toxin Sequence:**

Cys-Cys-Xaa3-Ala-Ala-Ala-Cys-Ala-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:355)

20 **Name:** Au3.2  
**Species:** aulicus  
**Cloned:** Yes

**DNA Sequence:**

30 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTTCCGTTACTGCTCTTCCGCCGGATGGAGATCAACCTGCAGACCG  
AGCTGCAGAGCGTAGGCAGGTCGAGCAGCATCCCGTGTTTGATCATGAAAGAGGGT  
GTTGCTCGCCACCATGCCACAGTATTTGCGCTGCTTTCTGTTGCGGGTGATGATAAC  
GTGTTGATGACCCACTTTGTCATCACGGCTGCGTCAAGTGTCTAATGAATAAGTAAA  
35 ATGATTGCAGT (SEQ ID NO:356)

**Translation:**

MMSKLGVLLTICLLLF SVTALPPDGDQPADRAAERRQVEQHPVFDHERGCCSPPCHSIC  
AAFCCG (SEQ ID NO:357)

**Toxin Sequence:**

Gly-Cys-Cys-Ser-Xaa3-Xaa3-Cys-His-Ser-Ile-Cys-Ala Ala-Phe-Cys-Cys-# (SEQ ID NO:358)

45 **Name:** Au3.3  
**Species:** aulicus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
 TCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTTGATGGAGATCAACATGCAGACCAA  
 5 CCTGCAGAGCGTCTGCAGGGCGACATTTTATCTGAAAAGCATCCCTTATTTAATCCC  
 GTCAAACGGTGTGTCGACCGGTGGCATGTGCCATGGGATGCAAGCCTTGTTGTGG  
 ATGAGCAGCTTTGTTATCGTGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGATT  
 GCAGT (SEQ ID NO:359)

**Translation:**

MMSKLGVLITICLLLFSLTAVPLDGDQHADQPAERLQGDILSEKHPLFNPVKRCCRPVA  
 CAMGCKPCCG (SEQ ID NO:360)

**Toxin Sequence:**

Cys-Cys-Arg-Xaa3-Val-Ala-Cys-Ala-Met-Gly-Cys-Lys-Xaa3-Cys-Cys-# (SEQ ID NO:361)

**Name:** Au3.4

**Species:** aulicus

**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCaTGATGTCTAAACTGGGAGTCTTGTTGATCATCTG  
 TCTACTTCTGTCTCCCCTTACTGCTGTTCCGCTGGATGGAGATCAACCTGCAGACCG  
 25 ACCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAACATCAACCCATGTTTGATGC  
 CATCAGACAGTGTTGCCCGGCGGTGGCATGCGCCATGGGATGCGAGCCTTGTTGTG  
 GATGACCAGCTTTGTTATCGCGGCCTCATCAAGTGTCTAATGAATAAGTAAAATGAT  
 TGCAGT (SEQ ID NO:362)

**Translation:**

MMSKLGVLIIICLLLSPLTAVPLDGDQPADRPAERMQDDISSEHQPMFDAIRQCCPAVA  
 CAMGCEPCCG (SEQ ID NO:363)

**Toxin Sequence:**

35 Xaa2-Cys-Cys-Xaa3-Ala-Val-Ala-Cys-Ala-Met-Gly-Cys-Xaa1-Xaa3-Cys-Cys-# (SEQ ID  
 NO:364)

**Name:** Ae3.1

**Species:** aureus

**Cloned:** Yes

**DNA Sequence:**

CAAGAAGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
 45 GTCTACTTCTGTTTTCCCTTACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
 AACATGCAGAGCGTCTGCATGACCGCCTTCCAAGTAAAATCATCCCTTATATGATC  
 CCGTCAAACGGTGTGCGATGATTCGGAATGCGACTATTCTTGCTGGCCTTGCTGTA

TTTTTGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAAC  
GATTGCAGT (SEQ ID NO:365)

**Translation:**

5 MMSKLGALLTICLLLFSLTAVPLDGDQHADQHAERLHDLPTENHPLYDPVKRCCDDS  
ECDYSCWPCCIFG (SEQ ID NO:366)

**Toxin Sequence:**

10 Cys-Cys-Asp-Asp-Ser-Xaa1-Cys-Asp-Xaa5-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Ile-Phe-# (SEQ ID  
NO:367)

**Name:** Ae3.2  
**Species:** aureus  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGCCTTGTTGACCATCT  
GTCTACTTCTGTTTTCCCTAACTGCTGTTCCGCTGGATGGAGATCAACATGCAGACC  
AACCTGCAGAGCGTCTGCAGGACCGCATTCCTCAACTGAAAATCATCCCTTATTTGATC  
CGAACAAACGGTGTTGCAATGATTGGGAATGCGACGATTCATGCTGGCCTTGCTGTT  
ATGGATAACCTTTGTTATCGCGGCCTCATCAAGTGTCAAATGAATAAGTAAAACGAT  
TGCAGT (SEQ ID NO:368)

**Translation:**

MMSKLGALLTICLLLFSLTAVPLDGDQHADQPAERLQDRIPTENHPLFDPNKRCCNDWE  
CDDSCWPCCYG (SEQ ID NO:369)

**Toxin Sequence:**

30 Cys-Cys-Asn-Asp-Xaa4-Xaa1-Cys-Asp-Asp-Ser-Cys-Xaa4-Xaa3-Cys-Cys-Xaa5-# (SEQ ID  
NO:370)

**Name:** Cn3.1  
**Species:** consors  
**Cloned:** Yes

**DNA Sequence:**

40 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCAATGGATGGAGATCAATCTGTAGACCGA  
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCTGCATCCCTTGTTCAATCAG  
AAAAGAATGTGTTGCGGCGAAGGTGCGCCATGCCCCAGCTATTTTCAGAAACAGTCA  
GATTTGTCATTGTTGTTAAATGACAACGTGTCGATGACCAACTTCGTTATCACGACT  
AATGAATAAGTAAAATGATTGCAGT (SEQ ID NO:371)

**Translation:**

MMSKLGVLLTICLLLFPLTALPMDGDQSVDRPAERMQDDISSELHPLFNQKRMCCGEG  
APCPSYFRNSQICHCC (SEQ ID NO:372)

**Toxin Sequence:**

5 Met-Cys-Cys-Gly-Xaa1-Gly-Ala-Xaa3-Cys-Xaa3-Ser-Xaa5-Phe-Arg-Asn-Ser-Gln-Ile-Cys-His-  
Cys-Cys-^ (SEQ ID NO:373)

**Name:** Cn3.3  
**Species:** consors  
**Cloned:** Yes

**DNA Sequence:**

TAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACCATCTG  
TCTGCTTCTGTTTCCCCTTATTGCTCTTCCAATGGATGGAGATCAACCTGCAGACCGA  
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTCAGCAGCATCCCTTGTTTGATAAG  
AGAGGCCGCTGTTGCGATGTGCCGAACGCATGCTCCGGCAGATGGTGCAGAGATCA  
CGCACAATGTTGCGGATGACGATAACGTGTTGATGACCAACTTTGTGATCACGGCTA  
CATCAAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:374)

**Translation:**

MMSKLGVLLTICLLLFPLIALPMDGDQPADRPARMQDDISSQQHPLFDKRGRCCDVPN  
ACSGRWCRDHAQCCG (SEQ ID NO:375)

**Toxin Sequence:**

Gly-Arg-Cys-Cys-Asp-Val-Xaa3-Asn-Ala-Cys-Ser-Gly-Arg-Xaa4-Cys-Arg-Asp-His-Ala-Gln-  
Cys-Cys-# (SEQ ID NO:376)

**Name:** Cn3.4  
**Species:** consors  
**Cloned:** Yes

**DNA Sequence:**

CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGTTGACTGTCTG  
TTTGCTTCTGTTTCCCCTTACTGCTCTTCCGATGGATGGAGATCAACCTGCAGACCAA  
CCTGCAGAGCGTATGCAGGACGACATTTTCATCTGAGCAGCATCCCTTGTTTGATAAG  
AGACAAAGGTGTTGCACTGGGAAGAAGGGGTCATGCTCCGGTAAAGCATGCAAAA  
GTCTCAAATGTTGCTCTGGACGATAACGTGTTGATGACCAACTTTGTTATCACGGCT  
ACGTCAAGTGTCTAGTGAATAAGTAAAACGATTGCAGT (SEQ ID NO:377)

**Translation:**

MMSKLGVLLTVCLLLFPLTALPMDGDQPADQPAERMQDDISSEQHPLFDKRQRCCTGK  
KGSCSGKACKSLKCCSGR (SEQ ID NO:378)

**Toxin Sequence:**



Xaa2-Arg-Cys-Cys-Thr-Gly-Lys-Lys-Gly-Ser-Cys-Ser-Gly-Lys-Ala-Cys-Lys-Ser-Leu-Lys-Cys-Cys-Ser-# (SEQ ID NO:379)

5 **Name:** Em3.1  
**Species:** emaciatus  
**Cloned:** Yes

**DNA Sequence:**

10 CAAGAGGGATCGATAGCAGTTCATGATGTCTAAACTGGGAGTCTTGCTGACCATCTGTCTGCTTCTGTT  
 TCCCCTTACTGTTCTTCCGATGGATGGAGATCAACCTGCAGACCTACCTGCATTGCGTGCGCAGTTCTT  
 TGCACCTGAACATAGTCCCCGGTTTGACCCCGTCAAACGGTGCTGCTCGCGGGATTGCAGTGTTCAT  
 CCCTTGTTGCCCGTATGGATCACCTTGATTATTGCGGCCACGTCAAGTGTCTAATGAATAAGTAAAATG  
 ATTGCAGT (SEQ ID NO:380)

**Translation:**

MMSKLGVLITICLLFPLTVLPMDGDQPADLPALRAQFFAPEHSPRFDPVKRCCSRDCSVCIPCCPYGSP  
 (SEQ ID NO:381)

**Toxin Sequence:**

Cys-Cys-Ser-Arg-Asp-Cys-Ser-Val-Cys-Ile-Xaa3-Cys-Cys-Xaa3-Xaa5-Gly-Ser-Xaa3-^ (SEQ ID NO:382)

Where:

Xaa1 is Glu or  $\gamma$ -carboxy-Glu

Xaa2 is Gln or pyro-Glu

Xaa3 is Pro or hydroxy-Pro

Xaa4 is Trp or bromo-Trp

Xaa5 is Tyr,  $^{125}\text{I}$ -Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

^ is free carboxyl or amidated C-terminus, preferably free carboxyl

# is free carboxyl or amidated C-terminus, preferably amidated

? = Status of C-term not known.

TABLE2

Alignment of  $\mu$ -Conopeptides (SEQ ID NO:)

TYPE 1

40	A3.4 (F283)	---CCKVQ-CES--C---TPCC^ (383)
	Ak3.1 (F585)	---CCELP-CC~7FC---VPCC^ (384)
	Ar3.1	---CCERP-CNIG-C---VPCC^ (385)
	Bn3.1 (F586)	---CCNWP-CSMG-C---IPCCYY^ (386)
	Bt3.1	---CCELP-CH-G-C---VPCCWP^ (387)
45	Bt3.2	---CCGLP-CN-G-C---VPCCWPS^ (388)
	Bt3.3	---CCSRN-CAV--C---IPCCPNWPA^ (389)
	bt3a	---CCKQS-CTT--C---MPCCW^ (390)

	bt3b	--ACCXQS-CTT--C---MPCC^ (391)
	bt3c	---CCEQS-CTT--C---MPCCW? (392)
	Ca3.3	R--CCRYP-CPDS-C--HGSCCYK^ (393)
	Ca3.4	---CCPPVACNMG-C---KPCC# (394)
5	Ca3.5	---CCDDSECDYS-C---WPCCMF# (395)
	Ca3.6 (F349)	---CCRR--CYMG-C---IPCCF^ (396)
	Circling	---CCPPVACNMG-C---KPCCG^ (397)
	Comatose/Death	SKQCCHLAACRFG-C---TOCCN^ (398)
	Cp3.1 (F594)	S--CCR--DCGED-C---VGCCR^ (399)
10	Ct3.1 (Z726)	---CCDWP-CIPG-C---TPCCLP^ (400)
	Da3.1	---CCDDSECDYS-C---WPCCILS^ (401)
	Da3.2	Z--QCCPPVACNMG-C---EPCC# (402)
	Da3.3	---CCNAGFCRFG-C---TPCCW^ (403)
	Di3.1	Z--CCVHP-C-P--C---TPCCR^ (404)
15	Fi3.1	---CCPWP-CNIG-C---VPCC^ (405)
	Fi3.2	---CCSKN-CAV--C---IPCCP^ (406)
	Fi3.3	---CCRWP-CP-ARC---GSCCL^ (407)
	Fi3.4	---CCELSRCL-G-C---VPCCTS^ (408)
	Fi3.5	---CCELSKCH-G-C---VPCCIP^ (409)
20	Ge3.1 (F590)	Z--CCTF--CNFG-C---QPCCVP^ (410)
	Ge3.2 (F343/Z734)	Z--CCTF--CNFG-C---QPCCLT^ (411)
	Ge3.3 (F590)	Z--CCTF--CNFG-C---QPCCVP^ (412)
	Gm3.1	---CCDDSECDYS-C---WPCCMF# (413)
	Gm3.2	G--CCHLLACRFG-C---SPCCW^ (414)
	Gm3.3	---CCSWDVCDHPSC---T-CCG# (415)
	La3.1	---CCDWP-CS-G-C---IPCC^ (416)
	Lp3.1 (F340)	ZINCCPWP-CPST-C--RHQCCH^ (417)
	Lv3.1 (F341)	ZINCCPWP-CPDS-C--HYQCCH^ (418)
	Mr3.2	---CCRLS-CGLG-C---HPCC# (419)
30	Mr3.3	--ECCGSFACRFG-C---VPCCV^ (420)
	Mr3.4	SKQCCHLPACRFG-C---TPCCW^ (421)
	Mr3.5 (F286)	-MGCCPFP-CKTS-C--TTLCC# (422)
	Ms3.1 (Z738)	--ACCEQS-CTT--C---FPCC^ (423)
	Nb3.1 (F87)	---CCELP-CGPGFC---VPCC^ (424)
35	Pu3.1 (F339)	---CCN-S-CYMG-C---IPCCF^ (425)
	Qc3.1 (F342)	ZR-CCQWP-CPGS-C---RCCRT# (426)
	Qc3.2	ZR-CCRWP-CPGS-C---RCCRYR^ (427)
	Qc3.3	R--CCRYP-CPDS-C--HGSCCYK^ (428)
	QcIIIA	---CCSQD-CLV--C---IOCCPN# (429)
40	QcIIIB	---CCSRH-CWV--C---IOCCPN? (430)
	Ra3.1 (F351)	Z-TCCS-N-CGED-C---DGCCQ^ (431)
	Scratcher I	---CCR-T-C-FG-C---TOCC# (433)
	Ts3.1 (F592)	---CCH-K-CYMG-C---IPCCI^ (434)
	Ts3.2 (F345)	K--CCRPP-CAMS-C-GMARCCY^ (435)
45	Bt3.5 (Z495)	R--CCRWP-CPSI-C-GMARCCFVMITC^ (436)
	Bt3.6 (Z497)	R--CCRWP-CP-SRC-GMARCCFVMITC^ (437)
	Tx3.1	F--CCDSNWCHISDC----ECCY# (438)

	U014	---	CCHWNWCDHL-C----	SCCGS^	(439)
	U017	--	DCCOLPACPFG-C---	NOCC#	(440)
	U019	---	CCAPSACRLG-C---	ROCCR^	(441)
	U020	---	CCAOSACRLG-C---	ROCCR^	(442)
5	U022	---	CCAPSACRLG-C---	RPCCR^	(443)
	U024	--	CCGSFACRFG-C---	VOCCV^	(444)
	U031	---	CCSWDVCDHPSC----	TCC#	(445)
	U032 (F353)	R--	CCKFP-CPDS-C--	RYLCC#	(446)
	Ae3.1	---	CCDDSECDYS-C---	WPCCIF#	(447)
10	Ae3.2	---	CCNDWECDDS-C---	WPCCY#	(448)
	Af3.1	R--	CCR-FPCPDT-C---	RHLCC#	(449)
	Af3.2	---	CC--MTC-FG-C---	TPCC#	(450)
	Af3.3	---	CCDDSECDYS-C---	WPCCIFS^	(451)
	Af3.4	---	CCR-LLC-LS-C---	NPCC#	(452)
15	Af3.6	---	CCDDSECGYS-C---	WPCCY#	(453)
	Au3.2	G--	CCS-PPCHSI-C--	AAFCC#	(454)
	Au3.3	---	CCRPVACAMG-C---	KPCC#	(455)
	Au3.4	Z--	CCPAVACAMG-C---	EPCC#	(456)
	Em3.1	---	CCS-RDC-SV-C---	IPCCPYGSP^	(457)
20	Ep3.1	---	CCDEDECNSS-C---	WPCCW#	(458)
	Ep3.2	---	CCDEDECSSS-C---	WPCCW#	(459)
	Ep3.3	---	CCPAAACAMG-C---	KPCC#	(460)
	Om3.1	---	CCDEEECSSA-C---	WPCCW#	(461)
	Om3.3	---	CCHLLACRFG-C---	SPCCW^	(462)
25	Sf3.1	---	CC--PRC-SE-C---	NPCC#	(463)

TYPE 2

30	Pn3.2 (AA049)	-RCC--	KFP-CPDS-C--	KYLCC#	(464)
	Fd3.2 (Z831)	-RCC--	RWP-CPSI-C-	GMARCCSS^	(465)
	Pu3.3 (AA405)	--	CC--KLL-CYSG-C---	TPCCHI^	(466)
	Eb3.1 (Z821)	--	CC--EQP-CYMG-C---	IPCCF^	(467)
	Eb3.2 (Z822)	--	CC--AQP-CYMG-C---	IPCCF^	(468)
35	Pu3.2 (AA403)	--	CC--V-S-CYMG-C---	IPCCF^	(469)
	Mf3.1 (Z882)	--	CC--DWP-CSAG-C---	YPCCFP^	(470)
	Mf3.2 (Z885)	-GCC--	PPM-C-TP-C---	FPCCFR^	(471)
	Ra3.2 (AA414)	RGCCAPPRK-CKDRACK-PARCCGP#			(472)
	Sm3.3 (AA419)	ZRCCNGRRG-CSSRWCRDHSRCC#			(473)
40	Cn3.3	GRCCDVPNA-CSGRWCRDHAQCC#			(474)
	Cn3.4	ZRCCTGKKGSCSGKACKSL-KCCS#			(475)

TYPE 3

45	A3.1	-MCCGEGRKCPSYFRNSQICHCC^			(476)
	A3.2 (F84)	--	CCR--WPCPRQIDGEY-CGCCCL#		(477)
	Bu3.5	-RCCGEGLTCPRYWKNSQICACC^			(478)
	Ca3.1	--	CCGPGGSCPVYFRDNFICGCC^		(479)

	Cr3.1	RKCCGKDGPCPKYFKDNFICGCC^ (480)
	E3.1	--CCS--WPCPRYSNGKLVCFCCCL# (481)
	M3.2	--CCGPGGSCP VYFRDNFICGCC^ (482)
	M3.3	-MCCGESAPCPSYFRNSQICHCC^ (483)
5	M3.4	ZKCCGPGGSCP VYFTDNFICGCC^ (484)
	M3.5	ZKCCGPGGSCP VYFRDNFICGCC^ (485)
	S3.1	ZKCCGEGSSCPKYFKNNFICGCC^ (486)
	U001	ZKCCS--GGSCPLYFRDRLICPCC^ (487)
	U034	ZKCCGPGASCPRYFKDNFICGCC^ (488)
10	Cn3.1	-MCCGEGAPCPSYFRNSQICHCC^ (489)

TYPE 4

15	A3.3 (F83)	ZK--CCTGK---KGSCSGKACKNL-KCCS# (490)
	A3.5 (Z488)	ZK--CCTGR---KGSCSGKACKNL-KCCS# (491)
	Bu3.1	VTDRCCK----GKREC-GRWCRDHSRCC# (492)
	Bu3.1A	VGDRCCK----GKRGC-GRWCRDHSRCC# (493)
	Bu3.2	VGERCCK---NGKRGC-GRWCRDHSRCC# (494)
	Bu3.3	IVDRCCN-KGNGKRGC-SRWCRDHSRCC# (495)
	Bu3.4	VGLYCCRPKPNGQMMC-DRWCEKNSRCC# (496)
	Ca3.2	-RD-CCTPP---KK-CKDRQCKPQ-RCCA# (497)
	L3.1	GRD-CCTPP---RK-CRDRACKPQ-RCCG# (498)
	L3.2	ZRL-CCGFP---KS-CRSRQCKPH-RCC# (499)
	La3.2	-RD-CCTPP---KK-CRDRQCKPA-RCCG# (500)
	La3.3	RPP-CCTYD---GS-CLKESCMRK-ACC# (501)
	La3.3A	RPP-CCTYD---GS-CLKESCKRK-ACC# (502)
	$\mu$ -GIIIA	-RD-CCTOO---KK-CKDRQCKOQ-RCCA# (503)
	$\mu$ -GIIIB	-RD-CCTOO---RK-CKDRRCKOM-KCCA# (504)
30	$\mu$ -GIIIC	-RD-CCTOO---KK-CKDRRCKOL-KCCA# (505)
	$\mu$ -PIIIA	ZRL-CCGFO---KS-CRSRQCKOH-RCC# (506)
	M3.1	-RD-CCTPP---KK-CKDRQCKPQ-RCCA# (507)
	Mr3.1	RGG-CCTPP---RK-CKDRACKPA-RCCGP# (508)
	Nb3.2 (F582)	ZK--CCTGK---KGSCSGKACKNL-KCCS# (509)
35	Pr3.1 (Z500)	RGG-CCTPP---KK-CKDRACKPA-RCCGP# (510)
	Pr3.2 (Z501)	-RG-CCTPP---RK-CKDRACKPA-RCCGP# (511)
	R3.1	LOS-CCSLN---LRLCOVOACKRN-OCCT# (512)
	R3.2	ZQR-CCTVK----RICOVOACRSK-OCCKS^ (513)
	R3.3	RGG-CCTPP---RK-CKDRACKPA-RCCGP# (514)
40	Sm3.1	ZK--CCTGK---KGSCSGKACKNL-KCCS# (515)
	T3.1	H-G-CCKGO---EG-CSSRECROQ-HCC# (516)
	T3.2 (Y088)	H-G-CCEGP---KG-CSSRECRPQ-HCC# (517)
	Wi3.1 (M548)	LPS-CCDFE----RLCVVPACIRH-QCCT# (518)

45

Type 5

Om3.2	CCKYGWTCLLGCTPCDC^ (519)
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Om3 . 4

CCRYGWT CWLGCTPCGC^ (520)

Type 6

5 S3.2 (F352)

Z-NCCNGG-CSSKWCRDHARCC# (432)

## EXAMPLE 3

Effect of Intrathecal Administration of  $\mu$ -Conopeptides

10 [0087] Male C57 black mice (20-25g) are obtained from Charles River Laboratories. These mice and the animals are housed in a temperature controlled ( $23^{\circ} \pm 3^{\circ}$  C) room with a 12 hour light-dark cycle with free access to food and water. All animals are euthanized in accordance with Public Health Service policies on the humane care of laboratory animals.

[0088] Intrathecal (it) drug injections are performed as described (Hylden and Wilcox, 1980). A  $\mu$ -conopeptide or vehicle is administered in a volume of 5  $\mu$ l. Duration of hind-limb paralysis is assessed. This experiment reveals that injection of  $\mu$ -conopeptides into the intrathecal space of C57 black mice produced a paralysis of the animal. The animals in this experiment recovered fully.

## EXAMPLE 4

Effect of  $\mu$ -Conopeptides as a Local Anesthetic

25 [0089] Male Hartley guinea pigs (retired breeders) are obtained from Charles River Laboratories. The local anesthetic test is performed essentially as described (Bulbring and Wajda, 1945). On the day prior to test day, a patch on the back of the guinea pig is denuded of hair, first by shaving with electric clippers and subsequently with depilatory cream (Nair®). Depilatory cream is applied for five minutes and removed with a warm washcloth. The guinea pigs are dried and returned to their cages. On the following day, intradermal injections (0.1 ml vols) of lidocaine, bupivacaine, a  $\mu$ -conopeptide or vehicle (0.5% cyclodextran) are made into the denuded patch. The injection produced a raised wheal on the surface of the skin which is

30 circled with a felt-tipped pen. Typically, four injections are made on the back of each guinea pig. In some cases, guinea pigs are reused following at least one week of recovery and injecting into an unused portion of the skin. The stimulus consists of mild pin pricks (not hard enough to break the skin) with a 26G needle. The response is a localized skin twitch caused by contraction

of cutaneous muscles. A unit test consisted of six uniform pin pricks, 3-5 seconds apart, within the injected area. Unit scores range from 0 (complete anesthesia) to 6 (no anesthesia). For potency experiments, the unit test is repeated at each site at five minute intervals for 30 minutes, and unit test scores summed (with 36 representing no anesthesia to 0 representing complete anesthesia. For duration experiments, unit tests are performed as described over the course of several hours to days.

[0090]  $\mu$ -Conopeptides of the present invention produce a potent and long lasting local anesthetic effect in the intracutaneous wheal test in the guinea pig. As expected, bupivacaine has a slightly longer duration than lidocaine, consistent with clinical observations.

#### EXAMPLE 5

##### Muscle Relaxant Effect of $\mu$ -Conopeptides in Anesthetized Monkeys

[0091]  $\mu$ -Conopeptides are dissolved 0.9 percent saline at a concentration of 2 mg/ml. Rhesus monkeys are anesthetized with halothane, nitrous oxide and oxygen. The maintenance concentration of halothane is 1.0%. Arterial and venous catheters are placed in the femoral vessels for drug administration and recording of the arterial pressure. Controlled ventilation is accomplished via an endotracheal tube. Twitch and tetanic contractions of the tibialis anterior muscle are elicited indirectly via the sciatic nerve. Recordings of arterial pressure, electrocardiogram (lead I), heart rate, and muscle function are made simultaneously. Four to six animals received each listed compound. Four additional animals received succinylcholine chloride or d-tubocurarine chloride as controls. It is seen that the tested  $\mu$ -conopeptides generally provide similar or better results than those seen for succinylcholine chloride or d-tubocurarine chloride.

#### EXAMPLE 6

##### *In vivo* Activity of $\mu$ -Conopeptides in Pain Models

[0092] The anti-pain activity of  $\mu$ -conopeptides is shown in several animal models. These models include the nerve injury model (Chaplan, et al., 1997), the nociceptive response to s.c. formalin injection in rats (Codene, 1993) and an NMDA-induced persistent pain model (Liu, et al., 1997). In each of these models it is seen that the  $\mu$ -conopeptides and  $\mu$ -conopeptides derivatives have analgesic properties.

[0093] More specifically, this study evaluates the effect of intrathecal administration of  $\mu$ -conopeptides in mice models of nociceptive and neuropathic pain. For nociceptive pain, the effect of the  $\mu$ -conopeptides is studied in two different tests of inflammatory pain. The first is the formalin test, ideal because it produces a relatively short-lived, but reliable pain behavior that is readily quantified. There are two phases of pain behavior, the second of which is presumed to result largely from formalin-evoked inflammation of the hind paw. A  $\mu$ -conopeptide is administered 10 minutes prior to injection of formalin. The number of flinches and/or the duration of licking produced by the injection is monitored. Since the first phase is presumed to be due to direct activation of primary afferents, and thus less dependent on long term changes in the spinal cord,  $\mu$ -conopeptides are presumed to have greatest effect on the magnitude of pain behavior in the second phase.

[0094] The mechanical and thermal thresholds in animals that received an injection of complete Freund's adjuvant into the hind paw are also studied. This produces a localized inflammation including swelling of the hind paw and a profound decrease in mechanical and thermal thresholds, that are detected within 24 hours after injection. The changes in thresholds in rats that receive  $\mu$ -conopeptides are compared with those of rats that receive vehicle intrathecal injections.

[0095] An important issue is whether the drugs are effective when administered after the pain model has been established, or whether they are effective only if used as a pretreatment. Clearly, the clinical need is for drugs that are effective after the pain has developed. To address this issue, animals are studied in which  $\mu$ -conopeptides are administered repeatedly, after the inflammation (CFA) or nerve injury has been established. In these experiments, a  $\mu$ -conopeptide is injected daily by the intrathecal (i.t.) route. The mechanical and thermal thresholds (measured, respectively, with von Frey hairs in freely moving animals and with the Hargreave's test, also in freely moving animals) are repeated for a 2 to 4 week period after the injury is induced and the changes in pain measured monitored over time.

## EXAMPLE 7

### Effect of $\mu$ -Conotoxins in a Pain Model

[0096] Analgesic activity of  $\mu$ -conotoxins is also tested in pain models as follows.

[0097] Persistent pain (formalin test). Intrathecal (it) drug injections are performed as described by Hylden and Wilcox (1980). An  $\mu$ -conopeptide or vehicle is administered in a

volume of 5  $\mu$ l. Fifteen minutes after the i.t. injection, the right hindpaw is injected with 20  $\mu$ l of 5% formalin. Animals are placed in clear plexiglass cylinders backed by mirrors to facilitate observation. Animals are closely observed for 2 minutes per 5 minute period, and the amount of time the animal spent licking the injected paw is recorded in this manner for a total of 45-50 minutes. Results are expressed as licking time in seconds per five minutes. At the end of the experiment, all animals are placed on an accelerating rotorod and the latency to first fall was recorded.  $\mu$ -Conopeptides are found to be active in this model which is predictive of efficacy for treating neuropathic pain.

[0098] Acute pain (tail-flick). A  $\mu$ -conopeptide or saline is administered intrathecally (i.t.) according to the method of Hylden and Wilcox (1980) in a constant volume of 5  $\mu$ l. Mice are gently wrapped in a towel with the tail exposed. At various time-points following the i.t. injection, the tail is dipped in a water bath maintained at 54° C. and the time to a vigorous tail withdrawal is recorded. If there is no withdrawal by 8 seconds, the tail is removed to avoid tissue damage.

[0099] Neuropathic pain. The partial sciatic nerve ligation model is used to assess the efficacy of  $\mu$ -conopeptides in neuropathic pain. Nerve injury is produced according to the methods of Malmberg and Basbaum (1998). Animals are anesthetized with a ketamine/xylazine solution, the sciatic nerve is exposed and tightly ligated with 8-0 silk suture around 1/3 to 1/2 of the nerve. In sham-operated mice the nerve is exposed, but not ligated. Animals are allowed to recover for at least 1 week before testing is performed. On the testing day, mice are placed in plexiglass cylinders on a wire mesh frame and allowed to habituate for at least 60 minutes. Mechanical allodynia is assessed with calibrated von Frey filaments using the up-down method as described by Chaplan et al. (1994), and the 50% withdrawal threshold is calculated. Animals that did not respond to any of the filaments in the series are assigned a maximal value of 3.6 grams, which is the filament that typically lifted the hindlimb without bending, and corresponds to approximately 1/10 the animal's body weight.

[0100] The data obtained demonstrate that  $\mu$ -conopeptides have potent analgesic properties in three commonly used models of pain: acute, persistent/inflammatory and neuropathic pain models.



## EXAMPLE 8

Activity of  $\mu$ -Conopeptide S3.2 on Neuronal Sodium Channels

[0101]  $\mu$ -Conopeptide S3.2 was tested for activity on sodium channels as follows. S3.2 was administered to mice by intracerebroventricular (ICV) injection. Administration of S3.2 in this manner caused mice to show a spectrum of activity that is characteristic of all sodium channel blockers, including rapid loss of righting reflex, coma-like inactivity and spastic uncontrolled limb movement. Following intrathecal (it) administration to mice, S3.2 causes rapid hindlimb paralysis that spreads to include the entire body over a course of 10-20 minutes followed by death, presumably due to respiratory paralysis. However, unlike classic  $\mu$ -conopeptides, S3.2 has no significant activity following intravenous administration (iv) to mice. Classic  $\mu$ -conopeptides, such as GIIIA and PIIIA, cause rapid paralysis and death following iv administration, indicating their activity at skeletal muscle sodium channels. To confirm the selectivity of S3.2, 80 nmol was administered iv to rats. The effect of S3.2 was measured on skeletal muscle contraction, blood pressure and heart rate. S3.2 was found to have no effect on any of these parameters. Controls were performed using classical  $\mu$ -conopeptides, including Sm3.1, Sm3.3 and Bu3.1 described herein, also administered iv at 80 nmol. These control peptides caused a dramatic decrease in skeletal muscle contractility, as well as a significant drop in systemic blood pressure. Thus,  $\mu$ -conopeptide S3.2 surprisingly is selective for neuronal sodium channels. The most obvious difference between the S3.2 sequence and the sequences of these other peptides is a shortened first loop (the first loop between cysteine residues) which lacks a charged amino acid.

[0102] It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

BIBLIOGRAPHY

- Abiko, H. et al. (1986). *Brain Res.* **38**:328-335.  
Aldrete, J.A. et al. (1979). *Crit. Care Med.* **7**:466-470.  
Barnay, G. et al. (2000). *J. Med. Chem.*

- Bitan, G. et al. (1997). *J. Peptide Res.* **49**:421-426.
- Bodansky et al. (1966). *Chem. Ind.* **38**:1597-98.
- Bulbring, W. and Wajda, J. (1945). *J. Pharmacol. Exp. Ther.* **85**:78-84.
- Cartier, G.E. et al. (1996). *J. Biol. Chem.* **271**:7522-7528.
- 5 Chandler, P. et al. (1993). *J. Biol. Chem.* **268**:17173-17178.
- Chaplan S.R. (1994). *J Neuroscience Methods* **53**:55-63.
- Chaplan S.R. (1997). *J Pharmacol. Exp. Ther.* **280**:829-838.
- Clark, C. et al. (1981). *Toxicon* **19**:691-699.
- Codere, T.J. (1993). *Eur. J. Neurosci.* **5**:390-393.
- 10 Craik, D.J. et al. (1991). *Toxicon* **39**:43-60.
- Cruz, L.J. at al. (1976). *Verliger* **18**:302-308.
- Ettinger, L.J. et al. (1978). *Cancer* **41**:1270-1273.
- Goodman and Gilman's The Pharmacological Basis of Therapeutics*, Seventh Ed., Gilman, A.G. et al., eds., Macmillan Publishing Co., New York (1985).
- 15 Hammerland et al. (1992). *Eur. J. Pharmacol.* **226**:239-244.
- Heading, C. (1999). *Curr. Opin. CPNS Invest. Drugs* **1**:153-166
- Horiki, K. et al. (1978). *Chemistry Letters* 165-68.
- Hubry, V. et al. (1994). *Reactive Polymers* **22**:231-241.
- Hylden, J.L.K. and Wilcox, G. (1980). *Eur. J. Pharmacol.* **67**:313-316.
- 20 Kaiser et al. (1970). *Anal. Biochem.* **34**:595.
- Kapoor (1970). *J. Pharm. Sci.* **59**:1-27.
- Kornreich, W.D. et al. (1986). U.S. Patent No. 4,569,967.
- Luer, M.S. & Hatton, J. (1993). *Annals Pharmacotherapy* **27**:912-921.
- Liu, H. et al. (1997). *Nature* **386**:721-724.
- 25 Malmberg, A.B. and Basbaum, A.I. (1998). *Pain* **76**:215-222.
- Martinez, J.S. et al. (1995). *Biochem.* **34**:14519-14526.
- McIntosh, J. M. et al. (1998). *Methods Enzymol.* **294**:605-624.
- The Merck Manual of Diagnosis and Therapy*, 16 Ed., Berkow, R. et al., eds., Merck Research Laboratories, Rahway, N.J., pp. 1436-1445 (1992).
- 30 *Methoden der Organischen Chemie (Houben-Weyl): Synthese von Peptiden*, E. Wunsch (Ed.), Georg Thieme Verlag, Stuttgart, Ger. (1974).
- Nehlig, A. et al. (1990). Effects of phenobarbital in the developing rat brain. In *Neonatal Seizures*, Wasterlain, C.G. and Vertt, P. (eds.), Raven Press, New York, pp. 285-194.
- Nishiuchi, Y. et al. (1993). *Int. J. Pept. Protein Res.* **42**:533-538.

- Olivera, B.M. et al. (1984). U.S. Patent 4,447,356.
- Olivera, B.M. et al. (1985). *Science* **230**:1338-1343.
- Olivera, B.M. et al. (1990). *Science* **249**:257-263.
- Olivera, B.M. et al. (1996). U.S. Patent 5,514,774.
- 5 Ornstein, et al. (1993). *Biorganic Medicinal Chemistry Letters* **3**:43-48.
- Remington's Pharmaceutical Sciences*, 18th Ed. (1990, Mack Publishing Co., Easton, PA).
- Rivier, J.R. et al. (1978). *Biopolymers* **17**:1927-38.
- Rivier, J.R. et al. (1987). *Biochem.* **26**:8508-8512.
- 10 Sambrook, J. et al. (1989). *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
- Shon, K.-J. et al. (1994). *Biochemistry* **33**:11420-11425.
- Stewart and Young, *Solid-Phase Peptide Synthesis*, Freeman & Co., San Francisco, CA (1969).
- Vale et al. (1978). U.S. Patent 4,105,603.
- Troupin, A.S. et al. (1986). MK-801. In *New Anticonvulsant Drugs, Current Problems in Epilepsy 4*, Meldrum, B.S. and Porter, R.J. (eds.), John Libbey, London, pp. 191-202.
- Van de Steen, P. et al. (1998). *Critical Rev. in Biochem. and Mol. Biol.* **33**:151-208.
- White, H.S., et al. (1992). *Epilepsy Res.* **12**:217-226.
- White, H.S., et al. (1995). Experimental Selection, Quantification, and Evaluation of Antiepileptic Drugs. In *Antiepileptic Drugs*, 4th Ed., Levy, R.H., eds., Raven Press, N.Y., pp. 99-110.
- 20 Wong, E.H.P. et al. (1986). *Proc. Natl. Acad. Sci. USA* **83**:7104-7108.
- Zhou L.M., et al. (1996). *J. Neurochem.* **66**:620-628.
- Zimm, S. et al. (1984). *Cancer Res.* **44**:1698-1701.
- U.S. Patent No. 3,842,067.
- 25 U.S. Patent No. 3,862,925.
- U.S. Patent No. 3,972,859.
- U.S. Patent No. 5,514,774.
- U.S. Patent No. 5,550,050.
- U.S. Patent No. 5,670,622.
- 30 U.S. Patent No. 5,719,264.
- U.S. Patent No. 5,844,077 (1998).
- Published PCT Application WO 92/19195.
- Published PCT Application WO 94/25503.
- Published PCT Application WO 95/01203.

Published PCT Application WO 00/23092.